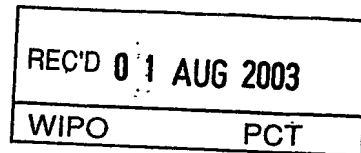


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## Prioritätsbescheinigung über die Einreichung einer Patentanmeldung

**Aktenzeichen:** 102 34 524.4

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**Anmelder/Inhaber:** oligene GmbH, Berlin/DE  
(vormals: Pathoarray GmbH)

**Bezeichnung:** Nukleinsäurearray

**IPC:** C 12 Q 1/68

Die angehefteten Stücke sind eine richtige und genaue Wiedergabe der ursprünglichen Unterlagen dieser Patentanmeldung.

München, den 2. Juli 2003  
Deutsches Patent- und Markenamt  
Der Präsident  
Im Auftrag



Profsky

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## Beschreibung

Die Erfindung betrifft einen Array bestehend aus Oligo-  
5 oder Polynukleotidsonden, die immobilisiert auf einen  
festen Träger aufgebracht sind. Das Array ist dadurch  
charakterisiert, dass auf der Oberfläche Sequenzen einer  
Auswahl oder aller der in den Tabellen 1-6 genannten se-  
10 lektiven Monozyten-Makrophagen-Gene gebunden sind. Dieser  
Nukleinsäure-Array ermöglicht die Diagnose der rheumatoi-  
den Arthritis, eine begleitende Analyse der Behandlungseffektivität und die Überwachung von Nebenwirkungen bei  
15 der anti-Tumornekrosefaktor-(TNF)-Therapie und somit die  
Auswahl der für den jeweiligen Patienten mit rheumatoider  
Arthritis am wirkungsvollsten Therapie. Die vorliegende  
Erfindung betrifft ferner einen Nukleinsäure-Array zur  
Prognose und zur Entwicklung neuer anti-TNF gerichteter  
Pharmaka oder solcher Pharmaka, die in dessen Regelkreis  
eingreifen.

20 Die Zellen des Monozyten / Makrophagen-Systems sind an  
der Aktivierung und Aufrechterhaltung von Entzündungskas-  
kaden im Blut und im Gewebe z. B. im Rahmen der rheuma-  
toiden Arthritis und bei anderen chronisch entzündlichen  
Erkrankungen, aber auch bei autoaggressiven Erkrankungen  
wesentlich beteiligt. Bei diesen Erkrankungen sind Mono-  
zyten und Makrophagen hoch aktiviert, zeigen Veränderun-  
gen im Besatz ihrer Oberflächen-Moleküle, treten mit an-  
30 deren Zellen in Kontakt und sezernieren bestimmte Boten-  
stoffe wie u. a. TNF-alpha, die dafür sorgen, den Entzün-  
dungsvorgang zu unterhalten. TNF-alpha ist ein von Mono-  
zyten / Makrophagen, Lymphozyten und Mastzellen gebilde-  
tes Zytokin mit Einfluss auf Entzündung, Sepsis, Lipid-  
und Proteinstoffwechsel, Blutbildung, Angiogenese, Wund-

heilung und Immunabwehr, das aber auch zytolytische bzw. zytostatische Wirkung auf Tumorzellen hat.

Bei entzündlichen Erkrankungen zeigen Monozyten /

5 Makrophagen ein charakteristisches, pathologisch verändertes Genexpressionsmuster mit deutlichen Abweichungen im Vergleich zu gesunden Probanden. Mit dem Fachmann bekannten bioinformatischen Methoden wie z. B. der Signifikanz- und Clusteranalyse lassen sich u. a. Gene mit ähnlichem Verhalten und hoch- oder niederregulierte Gene aus  
10 den Hybridisierungsmustern eines Nukleinsäurearrays bestimmen.

Die zunehmende Verfügbarkeit der Hochdurchsatz-Verfahren  
15 in Form von Nukleinsäurearrays, die exponentiell anwachsenden Informationen zum humanen Genom und der Genexpression, sowie die globale Vernetzung von Datenbanken mit strukturierten biomedizinischen Informationen wird die Betrachtungsweise chronisch entzündlicher und entzündlich-rheumatischer Krankheitsbilder grundlegend verändern. Aus dem verbesserten Verständnis der molekularen Grundlagen der zell-, gewebs- und krankheitsspezifischen Genexpression lassen sich die molekularen Abläufe definieren und tragen dazu bei, eine frühere Diagnose und verbesserte Prognose zu erlauben. Zum anderen gewährleisten Mikroarray-Technologien effektivere Therapieformen für die rheumatoide Arthritis und für andere chronisch entzündliche Erkrankungen zu entwickeln und ermöglichen ein schnelles Screeningsystem. Ferner erlauben diese multiplen Verfahren die Entwicklung von pharmazeutischen und  
30 biologisch wirksamen Medikamenten (Biologicals) zu beschleunigen und die Testphasen der Medikamentenwirkung, wie auch die Beurteilung der Medikamenten Nebenwirkungen schneller beurteilen zu können. Aus diesem Grund stellt

dieses Verfahren einen volkswirtschaftlichen und wirtschaftlichen Gewinn dar.

Die Mikroarray Technologie stellt eine Miniaturisierung analytischer Verfahren auf der Basis der DNA- bzw. RNA-Hybridisierung im Hochdurchsatz-Verfahren dar. Gleichzeitig können dadurch viele tausend verschiedene DNA/DNA- (DNA/RNA-) Wechselwirkungen innerhalb eines Testansatzes analysiert werden. mRNA-Expressionsprofile werden mittels DNA-Arrays durch die Hybridisierung von markierten cRNA oder cDNA-Proben bestimmt. Diese Technologien erfordern ein hohes Maß an Automatisierung und Standardisierung mit Aufbau und Nutzung entsprechender Proben- und Datenbanken (Sequenzinformationen, Oligonukleotide). Die derzeit verwendeten DNA-Arrays unterscheiden sich im Trägermaterial (Nylonmembranen, Glasoberflächen, Edelmetall bedampfte Glasoberflächen, Kunststoffe), der Länge bzw. der Herstellung der an den Träger immobilisierten DNA-Sequenzen und der Markierungstechnik für eine zu bindende Probe. In Analogie zu den Methoden der DNA-Hybridisierung beim Southern-/Dot-Blot können DNA-Sequenzen auf einem Filter punktförmig und in systematischer Reihenfolge mit einem Druckkopf durch Spotting, durch Piezo-Druckverfahren (Tintenstrahltechnologie) oder durch Photolithographie (chemische Direktsynthese auf dem Trägermaterial) fixiert werden. Die DNA kann dabei eine cDNA, ein PCR-Produkt oder ein synthetisch hergestelltes Oligonukleotid sein. Jede dieser aufgetragenen Sequenzen ist damit einem spezifischen Ort in einer bekannten Anordnung zugeteilt. Aus einer klinischen oder aber pharmazeutisch zu untersuchenden Probe kann RNA aufgereinigt werden und nach Umschreibung durch reverse Transkription mit den auf dem Array befindlichen komplementären Nukleinsäurensträngen die in einer hohen genomweiten Anzahl oder aber einer bereits



vorselektionierten Anzahl aufgebracht sind hybridisiert werden. Die Markierung der Probe erfolgt dabei mittels eingebauter radioaktiver Nukleotide, über Biotin-Streptavidin Wechselwirkungen, Digoxigenin-Enzym Verstär-

5 kungen oder aber über direkte oder indirekte eingebaute Fluoreszenzfarbstoffe. Das Auslesen der Information erfolgt über die Intensität der Radioaktivität oder der Fluoreszenz an einem spezifischen Ort des Trägermaterials und lässt somit Rückschlüsse zu, welche relative Menge an  
10 spezifisch gebundener DNA- bzw. RNA-Sequenz in der markierten Probe vorhanden war.

Das An- und Abschalten von Genen ist Grundlage aller biologischen Prozesse und außerdem eine extrem sensitive  
15 Antwort auf veränderte äußere Bedingungen. Mit der Extraktion von RNA aus einer biologischen Probe, dem Einwirken von markierter cDNA oder RNA auf einen Nukleinsäure-Array (Hybridisierung) und dessen Analyse ist innerhalb kürzester Zeit eine große Fülle von Informationen  
20 über den Zustand der Zellen in der biologischen Probe unter veränderten Bedingungen möglich. Die auf der Hybridisierung von Nukleinsäuren beruhende Technologie hat den Vorteil einer extrem hohen Spezifität, Sensitivität und relativ leichten, schnellen Durchführbarkeit.

Geschieht das An- oder Abschalten von Genen in Monozyten/Makrophagen in nicht physiologischer Weise, so kann es die Ursache von entzündlichen Erkrankungen oder ein messbares Zeichen für diese sein. Die Therapie mit anti-  
30 TNF wirksamen Medikamenten sollte im Idealfall die pathologisch veränderte Genexpression in den betroffenen Zellen auf das Niveau von gesunden Patienten normalisieren.

Durch Untersuchung der Genexpressionsprofile ist zu erwarten, dass eine neue molekulare Charakterisierung der rheumatoiden Arthritis und anderer chronisch entzündlicher Erkrankungen möglich wird und damit eine Einteilung

5 in Subgruppen nach pathophysiologischen Besonderheiten erfolgt. Bei den entzündungshemmenden anti-TNF Therapien stehen somit prognostische Vorhersagen in Aussicht über die Agressivität im weiteren Verlauf. Dies würde bereits  
10 frühzeitig Einfluß auf die Wahl und Intensität der medikamentösen Therapie mit den bisher bekannten bei chronischen Entzündungen verwendeten Medikamenten, aber auch mit biologisch wirksamen TNF-Blockern ausüben. Zum anderen ergeben sich hieraus weitere Ansatzpunkte, um die Therapieform im Hinblick auf die potentiellen Nebenwirkungen durch Einflussnahme dieser Medikamente zu gestalten und die Auswirkung der Nebenwirkungen rechtzeitig abzuschätzen.

20 Durch anti-TNF gerichtete Therapien bei der rheumatoiden Arthritis und anderen chronisch entzündlichen oder autoaggressiven Erkrankungen wird zum einen eine potentielle Entstehung neoplastischer Veränderungen bis hin zur Tumorbildung diskutiert, zum anderen vermindert die anti-TNF Therapie die Immunabwehr, sodass bei den behandelten Patienten vermehrt Infektionen auftreten, u. a. Tuberkulose.

30 Mit Hilfe von Nukleinsäure-Array-Systemen kann die Expression tumorrelevanter Gene im Verlauf der anti-TNF Behandlung überprüft und somit frühzeitig Hinweise auf mögliche neoplastische Veränderungen geben, so dass einer beginnenden Tumorentwicklung rechtzeitig entgegengesteuert und die anti-TNF Therapie entsprechend angepasst oder falls nötig abgebrochen werden kann.

Der Erfindung liegt die Aufgabe zugrunde, Mittel zur Überwachung der Wirksamkeit sowie von Nebenwirkungen der anti-TNF Therapie zu schaffen, aber auch die Feindiagnos-

5 tik einer entzündlichen Erkrankung und damit die Auswahl der für den jeweiligen Patienten effektivsten Therapieform zu ermöglichen. Eine weitere Aufgabe der vorliegenden Erfindung besteht darin, die Wirksamkeit und Nebenwirkungen neuer anti-TNF gerichteter Pharmaka im Rahmen  
10 von klinischen Studien zu verfolgen. Erfindungsgemäß wird ein neuer Array geschaffen bestehend aus Oligo- oder Polynukleotidsonden, die immobilisiert auf einem festen Träger aufgebracht sind. Verglichen mit bisher bekannten genomweiten DNA-Chips ist der Vorteil der Erfindung eine  
15 Kostenersparnis bei der Herstellung des Nukleinsäurearrays, weil es überwiegend nur Gene enthält, die zur Lösung der Aufgabe der Erfindung interessant sind, was den Aufwand der Datenauswertung minimiert und damit verbillicht.

20 Erfindungsgemäß wird die Aufgabe durch einen Nukleinsäure-Array gelöst, auf dessen Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1 bis 6 genannten selektiven Monozyten-Makrophagen-Gene aufgebracht sind. Anhand des Gen- oder Sequenznamens oder der Accession-Nummer kann die Sequenz aus öffentlich zugänglichen Datenbanken, vorzugsweise GeneBank oder EMBL, ermittelt werden. Die Sequenzen der aus dem Array befindlichen Nukleinsäuren können aus Genen bestehen, deren Expressions-  
30 niveau durch eine anti-TNF wirksame Therapie verändert wird.

Gegebenenfalls können auf dem erfindungsgemäßen Nukleinsäure-Array weitere Gene vorhanden sein, vorteilhaft sol-

che, von denen bekannt ist, dass sie in jeder Zelle exprimiert werden und zur Grundausstattung der Zelle gehören. Die Gene, die für diese Nukleinsäuren codieren, werden üblicherweise als Haushalts- oder Housekeeping-

5 Gene bezeichnet und werden zur Normierung der erhaltenen Signale verwendet. Das Array kann die genannten Sequenzen in Form von DNA, komplementärer RNA oder chemisch modifizierten Nukleinsäuren, vorzugsweise PNA (protein nucleic acid) enthalten.

10

Bei den Genen oder Gensequenzen kann es sich um krankheits- und nebenwirkungsrelevante selektionierte Gene der rheumatoiden Arthritis oder anderer chronisch entzündlicher Erkrankungen handeln, vorzugsweise aus dem Monozyten/Makrophagen-Zellsystem. Gegebenenfalls können auf  
15 den Oberfläche des Arrays auch Allele, Derivate und/oder Splicingvarianten der Gen- oder Genteilsequenzen oder Oligomersequenzen vorliegen. Die Übereinstimmung der Sequenzen auf dem Array mit den entsprechenden Sequenzen in  
20 Tabelle 1-6 soll dabei mindestens 80 % in den Proteinkodierenden Abschnitten der mRNA betragen.

Der Träger, auf den die Nukleinsäuren aufgetragen werden, kann jeder Träger sein, der normalerweise für RNA- oder DNA Arrays verwendet wird. Die Verfahren zum Auftragen und Immobilisieren der Nukleinsäuren sind Stand der Technik und dem Fachmann bekannt. Zur Kopplung der genannten Sequenzen kann der Träger mit reaktiven Gruppen, Metallverbindungen oder Legierungen beschichtet sein. Die Gene  
30 oder Gensequenzen können beispielsweise durch Spottingverfahren, Immobilisierungsverfahren oder durch in-situ Syntheseverfahren von Oligomeren oder spiegelbildlich in Form von RNA aufgebracht werden.

Das erfindungsgemäße Array kann beispielsweise zur Messung der Monozyten/Makrophagen Aktivierung oder der Entzündungsaktivität im Blut oder Zellgewebe bei entzündlichen Erkrankungen, vorzugsweise der rheumatoiden Arthri-

5 tis verwendet werden. Das Array kann z. B. zur Früherkennung der genannten Erkrankungen bei genetisch vorbelasteten Patienten verwendet werden, noch bevor sich klinische Symptome manifestieren. Ein weiterer Einsatzbereich ist die Feindiagnostik, vorzugsweise die Einteilung von Pati-  
10 enten in Subgruppen, die jeweils eine unterschiedliche Therapie und unterschiedliche Medikamente benötigen. Das Array kann ferner zur Therapieüberwachung, zur Verfolgung von Nebenwirkungen, zur Erstellung einer Prognose und zur Identifizierung neuer pharmazeutischer Targets bei  
15 den genannten Erkrankungen verwendet werden.

Dazu werden den zu untersuchenden Patienten Blut oder Gewebeproben entnommen, aus denen RNA mit bekannten Standardtechniken isoliert und gegebenenfalls als Gesamt-RNA  
20 oder Poly A+-RNA weiterverwendet wird. Mit reverser Transkriptase kann die RNA in cDNA umgeschrieben und dabei mit einer Markierung versehen werden, z. b. einem Fluoreszenzfarbstoff, einem radioaktiven Nuklid oder einem Enzym wie alkalische Phosphatase. Daneben kann die RNA direkt markiert oder unmarkiert zur Hybridisierung des Nukleinsäure-Arrays eingesetzt werden. Nach Hybridisierung des Arrays mit den Nukleinsäureproben und nachfolgenden Waschschritten kann die Bindung der Probe an  
30 die auf dem Array befindlichen Sequenzen mit jedem geeigneten Verfahren analysiert werden. Im Falle einer Fluoreszenzmarkierung sind dies optische Verfahren, bei radioaktiv markieren Proben käme eine Autoradiographie zur Anwendung und bei einer Enzymmarkierung enzymatische

Nachweisverfahren, z. B. die Umsetzung eines farblosen Substrates zu einem farbigen Produkt.

Ein inverser Nachweis von festphasengebundener Total- o-

5 der mRNA mit den Sequenzen aus Tabelle 1-6 ist ebenfalls möglich. Dazu werden auf den RNA-Mikroarrays Blut- oder gewebspezifische RNA-Moleküle von bis zu 500 Patienten gebunden. Der qualitative / quantitative Nachweis der Transkriptmenge relevanter Gene erfolgt dann mit den in  
10 Tabelle 1-6 beschriebenen selektionierten Genen, Genabschnitten oder Oligomeren. Die RNA-Proben werden auf Kopplungsträger gespottet und setzen sich aus Total-RNA oder messenger-RNA zusammen. Die RNA dient dabei als Target für die aus DNA-Mikroarrays abgeleiteten hoch signi-  
15 fikant exprimierten Gene nach Tabelle 1-6, die als markierte Sonden zur Hybridisierung eingesetzt werden. Vorgeschlagen wird das Koppeln biotinylierter RNA oder messenger-RNA auf Streptavidin beschichteten Glasträgern (Slides). Nach Markierung der RNA mit Biotinderivaten,  
20 wird die RNA auf Poly-L-Lysin behandelten vorzugsweise aber auf mit Streptavidin beschichteten Glas- oder Plastikslides durch Spotting aufgebracht und getrocknet. Eine Degradation der RNA wird so verhindert. Alternativ bietet sich eine kovalente Kopplung der RNA durch Bindung an reaktive Trägermaterialien an, die vorzugsweise durch UV-Bestrahlung katalysiert wird. Zusätzlich ist eine multiple, gleichzeitige Markierung verschiedener Gene, Geneinheiten oder Oligomere mit verschiedenen Markierungsspezies, z.B. Radioaktivität, Fluoreszein, Digoxigenin  
30 und enzymatischen Markierungen vorteilhaft.

Parallel unterschiedliche Markierungen der Sonden mit unterschiedlichen Fluoreszenzfarbstoffen sind möglich. Alternativ sind enzymatische oder aber radioaktive Sonden-

markierungen zu nennen. Zur Quantifizierung und Qualitätskontrolle werden markierte Haushaltsgene (alpha-, beta, gamma-Aktin, GAPDH usw.) eingesetzt. Bevorzugt wird der Nachweis hier parallel und gleichzeitig mit maximal 50

5. Gensonden pro Ansatz gleichzeitig durchgeführt.

10 Neben der Vereinfachung der biometrischen Analyse durch Kopplung von RNA Spezies an Trägermaterialien erlaubt dieses System eine schnelle Diagnostik und bietet eine komplexe für den Patienten individuell schnelle Diagnostik, Prognostik und Therapiesteuerung. Insbesondere bei pharmakologischen Entwicklungsstrategien erlaubt das System eine schnelle Durchführung mit hohem Durchsatz.

- 15 Die folgenden Beispiele und Abbildungen dienen nur zur Erläuterung und beschränken in keiner Weise den Umfang der Erfindung.

#### 1. Isolierung von Monozyten

- 20 Im hier angewandten Verfahren wurde die Auswahl selektiver hochreiner Monozyten des peripheren Blutes benutzt, um eine Aussage 1.) zur Krankheitsspezifität, 2.) der Anwendung des Therapeutikums anti-TNF-alpha, als "Biological", 3.) im Vergleich zum Gesunden Probanden, als auch 4.) zur Bewertung von anti-TNF-alpha relevanten gendiagnostischen Möglichkeiten, zu ermöglichen. Dabei wurden die peripheren Blut-Leukozyten aus peripherem Blut durch eine Fikollgradienten-Dichtezentrifugation angereichert. Diese Fraktion, die individuell unterschiedliche Zusammensetzung aus Monozyten (5-12%), CD4+ T-Zellen (85-92%)  
30 %, CD8+ T-Zellen (5-10%), NK-Zellen (2-5%), basophilen und neutrophilen Granulozyten aufweist, wurde zur Gewinnung spezifischer Monozytenfraktionen weiteren Reinigungsschritten unterzogen. Hierbei kamen sowohl Negativ-

selektionen, bei denen sämtliche andere Zellfraktionen über magnetische Beads-Antikörper Wechselwirkungen entfernt werden, als auch Positivselektionen durch CD14+ Markierung über magnetische Beads oder aber FACS Zellsortierungsverfahren zum Einsatz. Bei beiden Verfahren ergaben sich Monozyten-Zellreinheiten von ca. 96 %.

## 2. RNA-Gewinnung

Die reinen Monozytenfraktionen wurden in RNA-Lysepuffer aufgenommen und die RNA dann über einen kommerziell erhältlichen RNA Reinigungskit (Qiagen) gereinigt. Die RNA wurde über etablierte cDNA Umschreibemethoden durch reverse Transkription in cDNA umgeschrieben und dann einem weiteren linearen Amplifikationsschritt durch das angewandte "Eberwine Protokoll" zur Herstellung von aRNA (amplifizierte RNA) unterzogen. Die Quantität und Qualität der RNA, cDNA, und aRNA wurde jeweils durch Gelelektrophorese, photometrische Bestimmung und über Messungen mit dem Bioanalyzer 2100 (Fa. Agilent) verifiziert.

## 3. Affymetrix Chip Hybridisierung

Für Expressionsanalysen werden im System der Firma Affymetrix spezifische direkt aus Datenbanksequenzen abgeleitete Oligonukleotide als DNA-Proben verwendet. Diese werden auf dem Array mit Targets aus fluoreszenz-markierten revers transkribierten Proben in Form von cDNA oder mit linear amplifizierten Proben in Form von aRNA hybridisiert.

Die Hybridisierung des genomweiten Affymetrix-Arrays (U-133A) und weitere Bearbeitung erfolgt maschinell unter Standardbedingungen nach Angaben des Herstellers Affymetrix in einem speziellen Hybridisierungs- und Waschgerät mit den speziellen Puffern. Genexpressionsmuster



werden nach Hybridisierung über das Verhältnis der Fluoreszenzintensitäten bei einer bestimmten Wellenlänge erstellt. Solche Hochdurchsatz-Expressionsanalysen erlauben Vergleiche der Expressionsmengen von Genen gleichzeitig

5 in gesunden und kranken Personen oder Vergleiche der Genexpression vor und nach Arzneimittelzugabe zur Risikoabschätzung (Pharma-/Toxikogenomik), zur Feindiagnostik und Abschätzung der Komplexität von Erkrankungen.

10

#### 4. Datenauswertung

Zum Einsatz kamen dabei aRNA Proben aus peripheren Blut-Monozyten 1.) gesunder Blutspender, 2.) chronisch aktiver Patienten mit rheumatoider Arthritis vor Behandlung und  
15 3.) nach Behandlung mit TNF-alpha Antikörpern. Der Behandlungserfolg wurde über laborklinisch eindeutige Parameter und nach den klinisch anzuwendenden Kriterien der internationalen gültigen Parameteruntersuchungen (ACR-Kriterien) abgeschätzt. Ziel und Zweck dieser Dreigruppenuntersuchung war es, charakteristische Genexpressionen  
20 in folgenden Gruppensdefinitionen festzustellen:

1.) Eine genregulatorische Krankheitsspezifität bei der aktiven unbehandelten rheumatoiden Arthritis, im Vergleich zur Genexpression gesunder Probanden.

2.) Eine genregulatorisch spezifische Interpretation der anti-TNF-alpha-Behandlung zu charakterisieren und eine Bewertung der Behandlung im Vergleich zur Genexpression der aktiven unbehandelten Krankheit und im Vergleich zur Genexpression der gesunden Probanden durchzuführen.

30

3.) Die Bewertung von Nebenwirkungen durch das Medikament="Biological" anti-TNF zu gewährleisten. Hierbei wurde die spezifische Genexpression der anti-TNF-alpha behandelten Patienten mit rheumatoider

5 Arthritis mit der Genexpression der unbehandelten selben Patienten, und der von gesunden Blutspender verglichen.

10 Die Bearbeitung und Messung der einzelnen Genexpressionen innerhalb des genomweiten humanen Affymetrix-Arrays (U-133A) erfolgte innerhalb des zugehörigen Affymetrix Hybridisierungs-/ Wasch- und Auslesegerät - System. Die Auswertung vollzieht sich in 4 Schritten:

15 1. Bestimmung der bei der Expressionsanalyse detektierten signifikanten Gene, z. B. durch die „Fold-Change Method“ oder SAM („Significance Analysis of Microarrays“).

20 2. Separation der signifikanten Gene in verschiedene Sub-Populationen auf der Grundlage der Untersuchung der Expressionseigenschaften dieser Gene mittels Cluster-Analyse mit Verfahren wie „Hierarchical Clustering“, „Self-Organizing Maps“ oder „k-Means-Clustering“.

30 3. Auswertung des Verhaltens der signifikanten Gene innerhalb der Cluster unter Einbeziehung der klinischen Informationen (rheumatoide Arthritis (RA), anti-TNF-Therapie) und nach den Erfahrungswerten von Spezialisten.

#### 4. Zuordnung der beteiligten Gene nach biologischen Pathways.

Allgemeines Verhalten der signifikanten Gene innerhalb der Cluster:

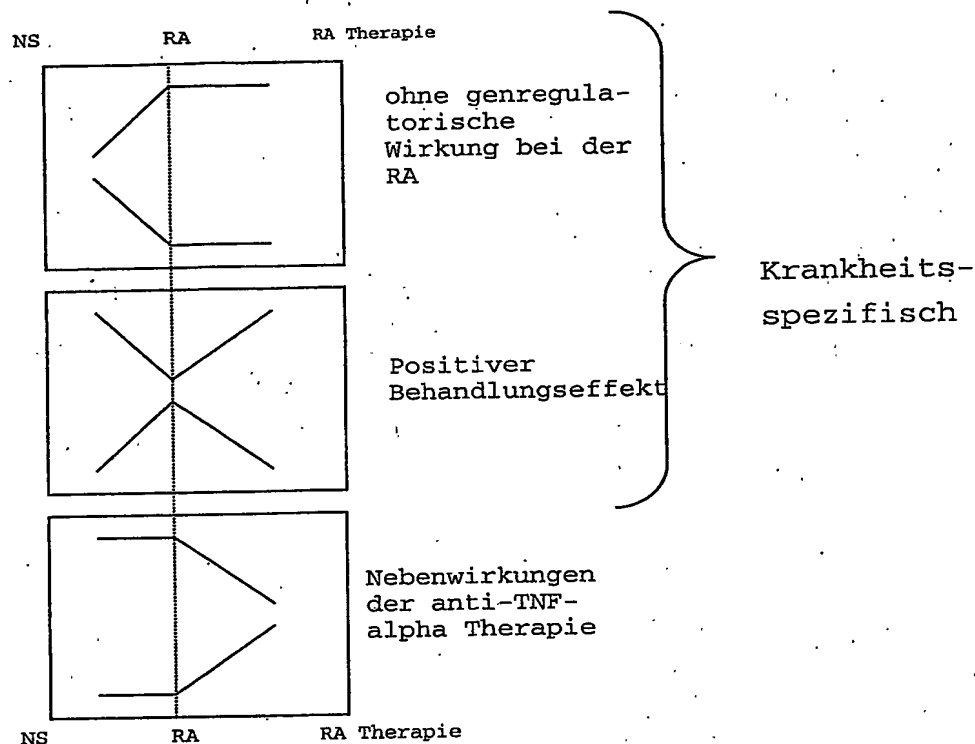
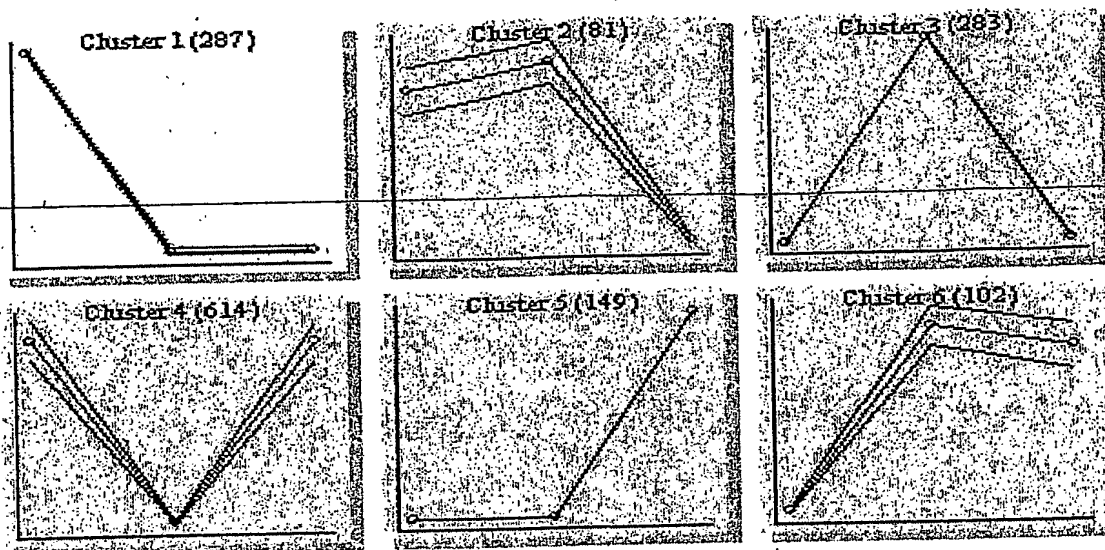


Abb. 1: schematische Darstellung der Clusteranalyse

Das Genexpressionsverhalten eines gesunden Normalspenders (NS) sowie und eines aktiven Patienten mit rheumatoider Arthritis (RA) vor und nach einer anti-TNF-alpha Therapie wurden mittels Clusteranalyse verglichen. Die Ergebnisse sind in den Abbildungen 1 und 2 dargestellt.



**Abb. 2: Clusteranalyse anhand realer Daten.**

Dargestellt sind die Genexpressionen der Clusteranalyse (n=6 Cluster). Die Anzahl der beteiligten Gene ist in Klammern wiedergegeben. Als Ergebnis der Clusteranalyse erhält man zusätzlich zum durchschnittlichen Genexpressions-Verhalten aller in einem Cluster befindlichen Gene ein Vertrauensintervall.

Die Cluster weisen dabei folgende Charakteristiken auf:

**CLUSTER-1:** Die krankheitsspezifische Genexpression ist kleiner im Vergleich zum Gesunden, die anti-TNF-Behandlung ist hier ohne genregulatorische Wirkung.

**CLUSTER-2:** Nebenwirkungen: Dargestellt durch die Medikamentenwirkung der Anti-TNF-alpha Behandlung besteht eine verminderte Expression der zugehörigen Gene beim behandelten Patienten.

**CLUSTER-3:** Die krankheitsspezifische Genexpression größer im Vergleich zum Gesunden. Die anti-TNF-alpha Behandlung zeigt einen positiven Effekt.

CLUSTER-4: Die krankheitsspezifische Genexpression ist kleiner im Vergleich zum Gesunden. Die anti-TNF-Behandlung zeigt einen positiven Effekt.

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5

CLUSTER-5: Nebenwirkungen: Dargestellt durch die Medikamentenwirkung der anti-TNF-alpha Behandlung besteht eine erhöhte Expression der zugehörigen Gene beim behandelten Patienten.

10

CLUSTER-6: Die krankheitsspezifische Genexpression ist größer im Vergleich zum Gesunden. Die anti-TNF-alpha Behandlung ist hier ohne genregulatorische Wirkung.

15

In den Tabellen 1-6 sind die in den oben beschriebenen Clustern enthaltenen Gene zusammen mit der Affymetrix Bezeichnung (links) und ihrer definierten GeneBank-Accession Nummer inkl. einer Beschreibung aufgeführt.

Tabelle 1: Gene aus Clusteranalyse 1

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
211654_x_at	gb:M17565.1 /DEF=Human MHC class II DQ-beta associated with DRw6, DQw1 protein, complete cds. /FEA=mrna /GEN=HLA-DQB1 /DB_XREF=gi:188188 /FL=gb:M17565.1
213831_at	Consensus includes gb:X00452.1 /DEF=Human mRNA for DC classII histocompatibility antigen alpha-chain. /FEA=mrna /PROD=DC classII histocompatibility antigenalpha-chain /DB_XREF=gi:32265 /UG=Hs.198253 major histocompatibility complex, class II, DQ alpha 1
212203_x_at	Consensus includes gb:BF338947 /FEA=EST /DB_XREF=gi:11285367 /DB_XREF=est:602036012P1 /CLONE-IMAGE:4184090 /UG=Hs.182241 interferon induced transmembrane protein 3 (I-8U)
209480_at	gb:M16276.1 /DEF=Human MHC class II HLA-DR2-Dw12 mRNA DQw1-beta, complete cds. /FEA=mrna /GEN=HLA-DRB2 /DB_XREF=gi:188397 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1 /FL=gb:M60028.1 gb:M17564.1 gb:M81140.1 gb:M81141.1 gb:M16276.1 gb:NM_002123.1
218345_at	gb:NM_018487.1 /DEF=Homo sapiens hepatocellular carcinoma-associated antigen 112 (HCA112), mRNA. /FEA=mrna /GEN=HCA112 /PROD=hepatocellular carcinoma-associated antigen 112 /FL=gb:AF258340.1 gb:NM_018487.1
221491_x_at	Consensus includes gb:AA807056 /FEA=EST /DB_XREF=gi:2876632 /DB_XREF=est:oc35c12.s1 /CLONE-IMAGE:1351702 /UG=Hs.279930 major histocompatibility complex, class II, DR beta 3 /FL=gb:M27635.1 gb:NM_022555.1 gb:M26038.1 gb:U95989.1 gb:U95819.1 gb:U66825.1
211734_s_at	gb:BC005912.1 /DEF=Homo sapiens, Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide, clone MGC:14507, mRNA, complete cds. /FEA=mrna /PROD=Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide /DB_XREF=gi:13543505 /FL=gb:BC005912.1
201330_at	gb:NM_002887.1 /DEF=Homo sapiens arginyl-trna synthetase (RARS), mRNA. /FEA=mrna /GEN=RARS /PROD=arginyl-trna synthetase /DB_XREF=gi:4506428 /UG=Hs.180832 arginyl-trna synthetase /FL=gb:BC000528.1 gb:NM_002887.1
201114_x_at	gb:NM_002792.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), mRNA. /FEA=mrna /GEN=PSMA7 /PROD=proteasome (prosome, macropain) subunit, alpha type, 7 /DB_XREF=gi:4506188 /UG=Hs.233952 proteasome (prosome, macropain) subunit, alpha type, 7 /FL=gb:BC004427.1 gb:AF022815.1 gb:AF054185.1 gb:NM_002792.1
213418_at	Consensus includes gb:NM_002155.1 /DEF=Homo sapiens heat shock 70KD protein 6 (HSP70B) (HSPA6), mRNA. /FEA=cds /GEN=HSPA6 /PROD=heat shock 70KD protein 6 (HSP70B) /DB_XREF=gi:4504514 /UG=Hs.3268 heat shock 70KD protein 6 (HSP70B) /FL=gb:NM_002155.1
208961_s_at	gb:AB017493.1 /DEF=Homo sapiens mRNA for DNA-binding zinc finger (GBF), complete cds. /FEA=mrna /PROD=DNA-binding zinc finger (GBF) /DB_XREF=gi:3582142 /UG=Hs.285313 core promoter element binding protein /FL=gb:BC000311.1 gb:BC004301.1 gb:AF001461.1 gb:AB017493.1 gb:NM_001300.2
217753_s_at	gb:NM_001029.1 /DEF=Homo sapiens ribosomal protein S26 (RPS26), mRNA. /FEA=mrna /GEN=RPS26 /PROD=ribosomal protein S26 /DB_XREF=gi:4506708 /UG=Hs.299465 ribosomal protein S26 /FL=gb:BC002604.1 gb:NM_001029.1
201403_s_at	gb:NM_004528.1 /DEF=Homo sapiens microsome glutathione S-transferase 3 (MGST3), mRNA. /FEA=mrna /GEN=MGST3 /PROD=microsome glutathione S-transferase 3 /DB_XREF=gi:4758713 /UG=Hs.111811 microsome glutathione S-transferase 3 /FL=gb:BC003034.1 gb:AF026977.1 gb:NM_004528.1
203103_s_at	gb:NM_014502.1 /DEF=Homo sapiens nuclear matrix protein NMP200 related to splicing factor PRP19 (NMP200), mRNA. /FEA=mrna /GEN=NMP200 /PROD=nuclear matrix protein NMP200 related to splicing factor PRP19 /DB_XREF=gi:7657380 /UG=Hs.173980 nuclear matrix protein NMP200 related to splicing factor PRP19 /FL=gb:NM_014502.1

221903_s_at	Consensus includes gb:BE046443 /FEA-EST /DB_XREF=gi:8363496 /DB_XREF=est:hn47d10.x2 /CLONE=IMAGE:3026803 /UG=Hs.18827 KIAA0849 protein
217379_at	Consensus includes gb:AL121934 /DEF=Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10) pseudogene, ESTs, STSs and GSSs /FEA-EST /DB_XREF=gi:9795199 /UG=Hs.272340 Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10) pseudogene, ESTs, STSs and GSSs
206120_at	gb:NM_001772.1 /DEF=Homo sapiens CD33 antigen (gp67) /CD33) mRNA. /FEA-mRNA /GEN=CD33 /PROD=CD33 antigen (gp67) / gb:NM_012321.1 /DEF=Homo sapiens U6 snRNA-associated Sm-like protein (LSM4) mRNA. /FEA-mRNA /GEN=LSM4 /PROD=U6 snRNA-associated Sm-like protein /DB_XREF=gi:6912485 /UG=Hs.76719 U6 snRNA-associated Sm-like protein /FL=gb:BC003652.1 gb:AF182290.1 gb:AF117235.1 gb:NM_012321.1 gb:AF251218.1
202737_s_at	Consensus includes gb:BG528420 /FEA-EST /DB_XREF=gi:13519957 /DB_XREF=est:602579853F1 /CLONE=IMAGE:4719060 / UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1
201416_at	Consensus includes gb:AW072388 /FEA-EST /DB_XREF=gi:6027386 /DB_XREF=est:xa07d05.x1 /CLONE=IMAGE:2567625 /UG=Hs.1583 neutrophil cytosolic factor 1 (47KD, chronic granulomatous disease, autosomal 1)
214084_x_at	gb:NM_004536.1 /DEF=Homo sapiens baculoviral IAP repeat-containing 1 (BIRC1) mRNA. /FEA-mRNA /PROD=baculoviral IAP re- peat-containing 1 /DB_XREF=gi:4758751 /UG=Hs.79019 baculoviral IAP repeat-containing 1 /FL=gb:U19251.1 gb:NM_004536.1
204861_s_at	gb:NM_004470.1 /DEF=Homo sapiens, clone MGC:10332, mRNA, complete cds. /FEA-mRNA /PROD=unknown protein for MGC:10332) / DB_XREF=gi:13325315 /UG=Hs.71869 apoptosis-associated speck-like protein containing a CARD /FL=gb:BC004470.1
221666_s_at	gb:NM_022766.1 /DEF=Homo sapiens hypothetical protein FLJ23239 (FLJ23239) mRNA. /FEA-mRNA /GEN=FLJ23239 /PROD=hypothetical protein FLJ23239
218421_at	gb:NM_018457.1 /DEF=Homo sapiens DKFZP564J157 protein (DKFZP564J157) mRNA. /FEA-mRNA /GEN=DKFZP564J157 / PROD=DKFZP564J157 protein /DB_XREF=gi:8922156 /UG=Hs.63042 DKFZP564J157 protein /FL=gb:AF217517.1 gb:NM_018457.1
217794_at	gb:NM_003610.1 /DEF=Homo sapiens RAE1 (RNA export 1, S.pombe) homolog (RAE1) mRNA. /FEA-mRNA /GEN=RAE1 / PROD=RAE1 (RNA export 1, S.pombe) homolog /DB_XREF=gi:4506398 /UG=Hs.196209 RAE1 (RNA export 1, S.pombe) homolog / FL=gb:U84720.1 gb:NM_003610.1
201558_at	gb:NM_018268.1 /DEF=Homo sapiens hypothetical protein FLJ10904 (FLJ10904) mRNA. /FEA-mRNA /GEN=FLJ10904 / PROD=hypothetical protein FLJ10904 /DB_XREF=gi:8922759 /UG=Hs.16470 hypothetical protein FLJ10904 /FL=gb:NM_018268.1
218055_s_at	Consensus includes gb:BE439987 /FEA-EST /DB_XREF=gi:9439470 /DB_XREF=est:HTM1-745F /UG=Hs.226133 growth arrest-specific 7 / FL=gb:AB007854.1 gb:NM_005890.1
202191_s_at	gb:NM_004899.1 /DEF=Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE) mRNA. /FEA-mRNA / GEN=BRE /PROD=brain and reproductive organ-expressed (TNFRSF1A modulator) /FL=gb:BC001251.1 gb:NM_004899.1 gb:L38616.1
205550_s_at	reproductive organ-expressed (TNFRSF1A modulator) (ubiquitinone) Flapovrotein 2 (24KD) /DB_XREF=gi:10835024 /UG=Hs.51299 NADH dehydrogenase (ubiquinone) Flapovrotein 2 (24KD) /FL=gb:NM_021074.1 gb:BC001632.1 gb:M22538.1
202941_at	gb:NM_020198.1 /DEF=Homo sapiens GK001 protein (GK001) mRNA. /FEA-mRNA /GEN=GK001 /PROD=GK001 protein / DB_XREF=gi:9910241 /UG=Hs.8207 GK001 protein /FL=gb:AF113221.1 gb:BC001300.1 gb:AF226054.1 gb:NM_020198.1
217814_at	Consensus includes gb:AA676803 /FEA-EST /DB_XREF=gi:2657325 /DB_XREF=est:zf65b04.s1 /CLONE=IMAGE:455119 / UG=Hs.13996 Homo sapiens CDNA: FLJ23260 fis, clone COL05804, highly similar to HSD90911 Human clone 23652 mRNA sequence
212051_at	Consensus includes gb:BF592782 /FEA-EST /DB_XREF=gi:11685106 /DB_XREF=est:7j94d06.x1 /CLONE=IMAGE:3442594 / UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212386_at	gb:NM_014169.1 /DEF=Homo sapiens HSPCL34 protein (HSPCL34) mRNA. /FEA-mRNA /GEN=HSPCL34 /PROD=HSPCL34 protein / DB_XREF=gi:7661793 /UG=Hs.279761 HSPCL34 protein /FL=gb:AF212243.1 gb:AF161483.1 gb:NM_014169.1
218571_s_at	gb:NM_003751.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 9 (eta, 116KD) (EIF3S9) mRNA. / FEA-mRNA /GEN=EIF3S9 /PROD=eukaryotic translation initiation factor 3, subunit 9 (eta, 116KD) /DB_XREF=gi:4503526 / UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116KD) /FL=gb:U62583.1 gb:NM_003751.1
203462_x_at	gb:NM_024300.1 /DEF=Homo sapiens hypothetical protein MGC2217 (MGC2217) mRNA. /FEA-mRNA /GEN=MGC2217 / PROD=hypothetical protein MGC2217 /DB_XREF=gi:13236525 /UG=Hs.323164 hypothetical protein MGC2217 /FL=gb:BC002546.1 gb:NM_024300.1
218642_s_at	

200024_at	gb:NM_001009.1 / DEF=Homo sapiens ribosomal protein S5 (RPS5), mRNA. / FEA=mrna / GEN=RPS5 / PROD=ribosomal protein S5 / DB_XREF=gi:4506728 / UG=Hs.76194 ribosomal protein S5 / FL=gb:NM_001009.1 gb:U14970.1
218101_s_at	gb:NM_004549.1 / DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) (NDUFC2), mRNA. / FEA=mrna / GEN=NDUFC2 / PROD=NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) / DB_XREF=gi:4758783 / UG=Hs.193313 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) / FL=gb:AF087659.1 gb:AF070652.1 gb:NM_004549.1
209329_x_at	gb:BC000587.1 / DEF=Homo sapiens, clone MGC:2198, mRNA, complete cds. / FEA=mrna / PROD=Unknown (protein for MGC:2198) / DB_XREF=gi:12653618 / UG=Hs.227152 mannan-binding lectin serine protease 1 (C4C2 activating component of Ra-reactive factor) / FL=gb:BC000587.1
208454_s_at	gb:NM_016134.1 / DEF=Homo sapiens aminopeptidase (LOC51670), mRNA. / FEA=CDS / GEN=LOC51670 / PROD=aminopeptidase / DB_XREF=gi:7706386 / UG=Hs.278993 aminopeptidase / FL=gb:AF107834.1 gb:NM_016134.1
214351_x_at	Consensus includes gb:AA789278 / FEA=EST / DB_XREF=gi:2849398 / DB_XREF=est:aj28510.s1 / CLONE=1391611 / UG=Hs.180842 ribosomal protein L13
207075_at	gb:NM_004895.1 / DEF=Homo sapiens chromosome 1 open reading frame 7 (C1ORF7), mRNA. / FEA=mrna / GEN=C1ORF7 / PROD=chromosome 1 open reading frame 7 / DB_XREF=gi:4757727 / UG=Hs.159483 chromosome 1 open reading frame 7 / FL=gb:AF054176.1 gb:NM_004895.1
201449_at	Consensus includes gb:AL567227 / FEA=EST / DB_XREF=gi:12920378 / DB_XREF=est:AL567227 / CLONE=CS0DF027VA11 (3 prime) / UG=Hs.239489 TIAL cytotoxic granule-associated RNA-binding protein / FL=gb:NM_022037.1 gb:M77142.1
213720_s_at	Consensus includes gb:AI831675 / FEA=EST / DB_XREF=gi:5452346 / DB_XREF=est:wj50903.x1 / CLONE=IMAGE:2406292 / UG=Hs.78202 SWINP related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
201593_s_at	Consensus includes gb:AV716798 / FEA=EST / DB_XREF=gi:10813950 / DB_XREF=est:AV716798 / CLONE=DCBAKE02 / UG=Hs.6375 uncharacterized hypothalamus protein HT010 / FL=gb:AF220184.1 gb:NM_018471.1
208095_s_at	gb:NM_001222.1 / DEF=Homo sapiens calcimulmodulin-dependent protein kinase (Cam kinase) II gamma (CAMK2G), mRNA. / FEA=mrna / GEN=CAMK2G / PROD=calcimulmodulin-dependent protein kinase (Cam kinase) II gamma / DB_XREF=gi:4502554 / UG=Hs.250857 calcimulmodulin-dependent protein kinase (Cam kinase) II gamma / FL=gb:U81554.1 gb:NM_001222.1
201173_x_at	gb:NM_006600.1 / DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. / FEA=mrna / GEN=NUDC / PROD=nuclear distribution gene C (A.nidulans) homolog / DB_XREF=gi:5729952 / UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog / FL=gb:BC002399.1 gb:BC003132.1 gb:AF130736.1 gb:AF125465.1 gb:AF100760.1 gb:NM_006600.1 (A.nidulans) homolog
217839_at	gb:NM_006070.1 / DEF=Homo sapiens TRK-fused gene (TFG), mRNA. / FEA=mrna / GEN=TFG / PROD=TRK-fused gene / DB_XREF=gi:5174718 / UG=Hs.250897 TRK-fused gene / FL=gb:NM_006070.1
203229_s_at	gb:NM_003993.1 / DEF=Homo sapiens CDC-like kinase 2 (CLK2), transcript variant phcl2, mRNA. / FEA=mrna / GEN=CLK2 / PROD=CDC-like kinase 2 isoform hcl2 / DB_XREF=gi:4502882 / UG=Hs.73986 CDC-like kinase 2 / FL=gb:NM_003993.1 gb:L29218.1
203656_at	gb:NM_014845.1 / DEF=Homo sapiens KIAA0274 gene product (KIAA0274), mRNA. / FEA=mrna / GEN=KIAA0274 / PROD=KIAA0274 gene product / DB_XREF=gi:7662033 / UG=Hs.10037 KIAA0274 gene product / FL=gb:DB7464.1 gb:NM_014845.1
218763_at	gb:NM_016930.1 / DEF=Homo sapiens syntaxin 18 (STX18), mRNA. / FEA=mrna / GEN=STX18 / PROD=syntaxin 18 / DB_XREF=gi:8394375 / UG=Hs.13406 syntaxin 18 / FL=gb:AB028741.1 gb:NM_016930.1
213846_at	Consensus includes gb:AA382702 / FEA=EST / DB_XREF=gi:2035020 / DB_XREF=est:EST95939 / UG=Hs.3462 cytochrome c oxidase subunit VIIC
201214_s_at	gb:NM_002712.1 / DEF=Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. / FEA=mrna / GEN=PPP1R7 / PROD=protein phosphatase 1, regulatory subunit 7 / DB_XREF=gi:4506012 / UG=Hs.36587 protein phosphatase 1, regulatory subunit 7 / FL=gb:BC000910.1 gb:NM_002712.1
216505_x_at	Consensus includes gb:AL118502 / DEF=Human DNA sequence from clone RP11-371L19 on chromosome 20 Contains a novel gene, a gene similar to the gene for ribosomal protein S10, ESTs, STSS, and CpG islands / FEA=mrna / GEN=mrna_3 / DB_XREF=gi:8894621 / UG=Hs.284299 Human DNA sequence from clone RP11-371L19 on chromosome 20 Contains a novel gene, a gene similar to the gene for ribosomal protein S10, ESTs, STSS, and CpG islands
203459_s_at	gb:NM_022575.1 / DEF=Homo sapiens vacuolar protein sorting 16 (yeast homolog) / DB_XREF=gi:12007657 / UG=Hs.302441 vacuolar protein sorting 16 (yeast homolog) / FL=gb:AF308801.1 gb:NM_022575.1
202880_s_at	gb:NM_004762.1 / DEF=Homo sapiens plectestrin homology, Sec7 and coiledcoil domains 1 (PSCD1), transcript variant 1, mRNA. / FEA=mrna / GEN=PSCD1 / PROD=cytohesin 1, isoform 1 / DB_XREF=gi:4758963 / UG=Hs.1050 plectestrin homology, Sec7 and coiledcoil domains 1 (cytohesin 1) / FL=gb:M85169.1 gb:NM_004762.1 gb:NM_017456.1



43511_s_at	Cluster Incl. AI201594:gc02h13.x1 Homo sapiens cDNA, 3' end / clone=IMAGE-1708487 / clone_end=3 / gb=AI201594 / gi=3754200 / ug=Hs.239333 / lens=591
203519_s_at	gb:NM_015542.1 / DEF=Homo sapiens regulator of nonsense transcripts 2; DKF2P434D222 protein (RENT2), mRNA. / FEA=mrna / GEN=RENT2 / PROD=regulator of nonsense transcripts 2 / DB_XREF=gi:11693131 / UG=Hs.3862 regulator of nonsense transcripts 2; DKF2P434D222 protein / FL=gb:AF301013.1 gb:NM_015542.1 gb:AV013249.1 gb:AF318574.1
206214_at	gb:NM_005084.1 / DEF=Homo sapiens phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) / DB_XREF=gi:4826883 / UG=Hs.93304 phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) / FL=gb:U24577.1 gb:NM_005084.1 gb:U20157.1
209933_s_at	gb:AF020314.1 / DEF=Homo sapiens CMRF-35-H9 mRNA, complete cds. / FEA=mrna / PROD=CMRF-35-H9 / DB_XREF=gi:4103065 / UG=Hs.9688 leukocyte membrane antigen / FL=gb:AF020314.1
202105_at	gb:NM_001551.1 / DEF=Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1), mRNA. / FEA=mrna / GEN=IGBP1 / PROD=immunoglobulin-binding protein 1 / DB_XREF=gi:4557662 / UG=Hs.3631 immunoglobulin (CD79A) binding protein 1 / FL=gb:BC004137.1 gb:NM_001551.1
218138_at	gb:NM_018848.1 / DEF=Homo sapiens McKusick-Kaufman syndrome (MKKS), mRNA. / FEA=mrna / GEN=MKKS / PROD=McKusick-Kaufman syndrome protein / DB_XREF=gi:9055271 / UG=Hs.46743 McKusick-Kaufman syndrome / FL=gb:AF275813.1 gb:AF221992.1 gb:AF221993.1 gb:NM_018848.1
220864_s_at	gb:NM_015965.1 / DEF=Homo sapiens CGI-39 protein; cell death-regulatory protein GRIM19 (LOC51079), mRNA. / FEA=mrna / GEN=LOC51079 / PROD=CGI-39 protein; cell death-regulatory protein GRIM19 / DB_XREF=gi:7705733 / UG=Hs.279574 CGI-39 protein; cell death-regulatory protein GRIM19 / FL=gb:AF132973.1 gb:AF155662.1 gb:NM_015965.1
213355_at	Consensus includes gb:AI989567 / FEA=EST / DB_XREF=gi:5836448 / DB_XREF=est:ws34e03.x1 / CLONE=IMAGE:2499100 / UG=Hs.34578 alpha2,3-sialyltransferase
212587_s_at	Consensus includes gb:AI809341 / FEA=EST / DB_XREF=gi:5395907 / DB_XREF=est:we96c09.x1 / CLONE=IMAGE:2348944 / UG=Hs.170121 protein tyrosine phosphatase, receptor type, C
205992_s_at	gb:NM_000585.1 / DEF=Homo sapiens interleukin 15 (IL15), mRNA. / FEA=mrna / GEN=IL15 / PROD=interleukin 15 / DB_XREF=gi:10835152 / UG=Hs.168132 interleukin 15 / FL=gb:NM_000585.1 gb:U14407.1
203262_s_at	gb:NM_004699.1 / DEF=Homo sapiens DNA segment on chromosome X (unique) 9928 expressed sequence (DXS9928E), mRNA. / FEA=mrna / GEN=DXS9928E / PROD=XAP-5 protein / DB_XREF=gi:4758219 / UG=Hs.54277 DNA segment on chromosome X (unique) 9928 expressed sequence / FL=gb:BC000028.1 gb:D83260.1 gb:AD001530.1 gb:NM_004699.1
213357_at	Consensus includes gb:AV701318 / FEA=EST / DB_XREF=gi:10717648 / DB_XREF=est:AV701318 / CLONE=ADAAGD10 / UG=Hs.278626 ArgAb1-interacting protein ArgBP2
207628_s_at	gb:NM_017528.1 / DEF=Homo sapiens putative methyltransferase (HASJ4442), mRNA. / FEA=mrna / GEN=HASJ4442 / PROD=putative methyltransferase / DB_XREF=gi:8923713 / UG=Hs.155020 putative methyltransferase / FL=gb:NM_017528.1
201527_at	gb:NM_004231.1 / DEF=Homo sapiens ATPase, vacuolar, 14 kD (ATP6S14), mRNA. / FEA=mrna / GEN=ATP6S14 / PROD=ATPase, vacuolar, 14 kD / DB_XREF=gi:4757819 / UG=Hs.78089 ATPase, vacuolar, 14 kD / FL=gb:D49400.1 gb:NM_004231.1
202282_at	gb:NM_004493.1 / DEF=Homo sapiens hydroxacyl-Coenzyme A dehydrogenase, type II (HADH2), mRNA. / FEA=mrna / GEN=HADH2 / PROD=hydroxacyl-Coenzyme A dehydrogenase, type II / DB_XREF=gi:4758503 / UG=Hs.171280 hydroxacyl-Coenzyme A dehydrogenase, type II / FL=gb:BC000372.1 gb:BC000829.1 gb:U73514.1 gb:U96132.1 gb:AF035555.1 gb:AF069134.1 gb:NM_004493.1
213735_s_at	Consensus includes gb:AI557312 / FEA=EST / DB_XREF=gi:4489675 / DB_XREF=est:PT2.1_16_E11.x / UG=Hs.1342 cytochrome c oxidase subunit Vb
212472_at	Consensus includes gb:BE965029 / FEA=EST / DB_XREF=gi:11768976 / DB_XREF=est:601658812R1 / CLONE=IMAGE:3886131 / UG=Hs.198793 Homo sapiens cDNA: FLJ22463 fls, clone HNC10126
214805_at	Consensus includes gb:U79273.1 / DEF=Human clone 23933 mRNA sequence. / FEA=mrna / DB_XREF=gi:1710239 / UG=Hs.239483 Human clone 23933 mRNA sequence
218084_x_at	gb:NM_014164.2 / DEF=Homo sapiens FYVD domain-containing ion transport regulator 5 (FYVD5), mRNA. / FEA=mrna / GEN=FYVD5 / PROD=related to ion channel / DB_XREF=gi:11612664 / UG=Hs.294135 FYVD domain-containing ion transport regulator 5 / FL=gb:NM_014164.2 gb:AF161462.1
218204_s_at	gb:NM_024513.1 / DEF=Homo sapiens FYVE and coiled-coil domain containing 1 (FYCOL), mRNA. / FEA=mrna / GEN=FYCOL / PROD=FYVE and coiled-coil domain containing 1 / DB_XREF=gi:13470091 / UG=Hs.257267 FYVE and coiled-coil domain containing 1 / FL=gb:NM_024513.1

200823_x_at	gb:NM_000992.1 /DEF=Homo sapiens ribosomal protein L29 (RPL29), mRNA. /FEA=mrna /GEN=RPL29 /PROD=ribosomal protein L29 /DB_XREF=gi:4506628 /UG=Hs.183698 ribosomal protein L29 /FL=gb:U49083.1 gb:NM_000992.1 gb:U10248.1
208968_s_at	gb:BC002568.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:2478, mRNA, complete cds. /FEA=mrna /PROD=hypothetical protein /DB_XREF=gi:12803484 /UG=Hs.4900 hypothetical protein /FL=gb:AF248964.1 gb:BC002568.1 gb:AF116609.1
208887_at	gb:BC000733.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 4 (delta, 44kd), clone MGC:2053, mRNA, complete cds. /FEA=mrna /PROD=eukaryotic translation initiation factor 3, subunit 4 (delta, 44kd) /DB_XREF=gi:12653882 /UG=Hs.28081 eukaryotic translation initiation factor 3, subunit 4 (delta, 44kd) /FL=gb:AF094850.1 gb:BC000733.1 gb:AF020833.1
214097_at	gb:U96074.1 gb:NM_003755.1 Consensus includes gb:AW024383 /FEA=EST /DB_XREF=gi:587793 /DB_XREF=est:WV03e06.x1 /CLONE=IMAGE:2528482 /UG=Hs.1948 ribosomal protein S21
212191_x_at	Consensus includes gb:AW574664 /FEA=EST /DB_XREF=gi:7246203 /DB_XREF=est:U1-HF-BL0-abw-q-10-0-UT.s1 /CLONE=IMAGE:3057859. /UG=Hs.180842 ribosomal protein L13
217957_at	gb:NM_013242.1 /DEF=Homo sapiens similar to mouse Glt3 or D. melanogaster transcription factor IIB (AF093680), mRNA. /FEA=mrna /GEN=AF093680 /PROD=similar to mouse Glt3 or D. melanogaster transcription factor IIB /DB_XREF=gi:8392874 /UG=Hs.279818 similar to mouse Glt3 or D. melanogaster transcription factor IIB /FL=gb:BC005152.1 gb:AF093680.1 gb:NM_013242.1
201658_at	Consensus includes gb:AU151560 /FEA=EST /DB_XREF=gi:11013081 /DB_XREF=est:AUI151560 /CLONE=NT2RP2005555 /UG=Hs.242894 ADP-ribosylation factor-like 1 /FL=gb:NM_001177.2 gb:L28997.1
218123_at	gb:NM_017835.1 /DEF=Homo sapiens chromosome 21 open reading frame 59 (C21ORF59), mRNA. /FEA=mrna /GEN=C21ORF59 /PROD=hypothetical protein FL320467 /DB_XREF=gi:8923436 /UG=Hs.5811 chromosome 21 open reading frame 59 /FL=gb:NM_021254.1 gb:BC000709.1 gb:NM_017835.1 gb:AF282851.1
205241_at	gb:NM_005138.1 /DEF=Homo sapiens SCO (cytochrome oxidase deficient, yeast) homolog 2 (SCO2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=SCO2 /PROD=SCO (cytochrome oxidase deficient, yeast) homolog 2 /DB_XREF=gi:4826991 /UG=Hs.278431 SCO (cytochrome oxidase deficient, yeast) homolog 2 /FL=gb:NM_005138.1
203740_at	gb:NM_005792.1 /DEF=Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /FEA=mrna /GEN=MPHOSPH6 /PROD=M-phase phosphoprotein 6 /DB_XREF=gi:5031918 /UG=Hs.152720 M-phase phosphoprotein 6 /FL=gb:BC005242.1 gb:NM_005792.1
221263_s_at	gb:NM_031287.1 /DEF=Homo sapiens hypothetical protein MGC3133 (MGC3133), mRNA. /FEA=mrna /GEN=MGC3133 /PROD=hypothetical protein MGC3133 /DB_XREF=gi:13775199 /FL=gb:NM_031287.1
218831_s_at	gb:NM_004107.1 /DEF=Homo sapiens Fc fragment of IgG, receptor, transporter, alpha (FCGR1), mRNA. /FEA=mrna /GEN=FCGR1 /PROD=Fc fragment of IgG, receptor, transporter, alpha /DB_XREF=gi:4758345 /UG=Hs.111903 Fc fragment of IgG, receptor, transporter, alpha /FL=gb:NM_004107.1 gb:U12255.1
201400_at	gb:NM_002795.1 /DEF=Homo sapiens proteasome (prosome; macropain) subunit, beta type, 3 (PSMB3), mRNA. /FEA=mrna /GEN=PSMB3 /PROD=proteasome (prosome; macropain) subunit, beta type, 3 /DB_XREF=gi:4506196 /UG=Hs.82793 proteasome (prosome; macropain) subunit, beta type, 3 /FL=gb:NM_002795.1 gb:D26598.1
203136_at	gb:NM_006423.1 /DEF=Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA. /FEA=mrna /GEN=RABAC1 /PROD=Rab acceptor 1 (prenylated) /DB_XREF=gi:5453959 /UG=Hs.11417 Rab acceptor 1 (prenylated) /FL=gb:NM_006423.1 gb:AF112202.1
205382_s_at	gb:NM_001928.1 /DEF=Homo sapiens D component of complement (adipsin) (DF), mRNA. /FEA=mrna /GEN=DF /PROD=adipsin complement factor D precursor /DB_XREF=gi:4503308 /UG=Hs.155597 D component of complement (adipsin) /FL=gb:M84526.1 gb:NM_001928.1
208714_at	gb:AF092131.1 /DEF=Homo sapiens 51kDa subunit of NADH dehydrogenase mRNA, complete cds. /FEA=mrna /PROD=51kDa subunit of NADH dehydrogenase /DB_XREF=gi:5138911 /UG=Hs.7744 NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD) /FL=gb:AF053070.1 gb:AF092131.1 gb:NM_007103.1
209224_s_at	gb:BC003674.1 /DEF=Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8), clone MGC:12315, mRNA, complete cds. /FEA=mrna /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) /DB_XREF=gi:13277539 /UG=Hs.163867 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) /FL=gb:BC003674.1 gb:AF047185.1 gb:NM_002488.1 gb:AF077029.1
210574_s_at	gb:AF241788.1 /DEF=Homo sapiens NP0011 (NP0011) mRNA, complete cds. /FEA=mrna /GEN=NP0011 /PROD=NP0011 /DB_XREF=gi:12005492 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:AF241788.1
214259_s_at	Consensus includes gb:AI144075 /FEA=EST /DB_XREF=gi:3665884 /DB_XREF=est:q161e12.x1 /CLONE=IMAGE:1861198 /UG=Hs.6980 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)

209234_at	Consensus includes gb:BF939474 /FEA=EST /DB_XREF=gi:12356794 /DB_XREF=est:nac76d12.x1 /CLONE=IMAGE:3440303 /UG=Hs.129908 KIAA0591 protein /FL=gb:BC001415.1
203654_s_at	gb:NM_004645.1 /DEF=Homo sapiens collin (COLL), mRNA. /FEA=mrna /GEN=collin /PROD=collin /UG=Hs.966 collin /FL=gb:U06632.1 gb:NM_004645.1
201129_at	gb:NM_006276.2 /DEF=Homo sapiens splicing factor, arginineserine-rich 7 (35kd) (SPRS7), mRNA. /FEA=mrna /GEN=SPRS7 /PROD=splicing factor, arginineserine-rich 7 (35kd) /DB_XREF=gi:6857827 /UG=Hs.184167 splicing factor, arginineserine-rich 7 (35kd) /FL=gb:BC000997.2 gb:122253.1 gb:NM_006276.2
202451_at	gb:BC000365.1 /DEF=Homo sapiens, general transcription factor IIIH, polypeptide 1 (62kd subunit), clone MGC:8323, mRNA, complete cds. /FEA=mrna /PROD=general transcription factor IIIH, polypeptide 1 (62kd subunit) /DB_XREF=gi:12653194 /UG=Hs.89578 general transcription factor IIIH, polypeptide 1 (62kd subunit) /FL=gb:BC000365.1 gb:BC004452.1 gb:NM_005316.1
218072_at	gb:NM_014186.1 /DEF=Homo sapiens HSPC166 protein (HSPC166), mRNA. /FEA=mrna /GEN=HSPC166 /PROD=HSPC166 protein /DB_XREF=gi:7661827 /UG=Hs.279836 HSPC166 protein /FL=gb:AL136688.1 gb:AF161515.1 gb:NM_014186.1
203063_at	gb:NM_014634.1 /DEF=Homo sapiens KIAA0015 gene product (KIAA0015), mRNA. /FEA=mrna /GEN=KIAA0015 /PROD=KIAA0015 gene product /DB_XREF=gi:7661861 /UG=Hs.278441 KIAA0015 gene product /FL=gb:DL3640.1 gb:NM_014634.1
204037_at	Consensus includes gb:BF055366 /FEA=EST /DB_XREF=gi:10809262 /DB_XREF=est:7j78f10.x1 /CLONE=IMAGE:3392587 /UG=Hs.75794 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1
218298_s_at	gb:NM_024952.1 /DEF=Homo sapiens hypothetical protein FLJ20950 (FLJ20950), mRNA. /FEA=mrna /GEN=FLJ20950 /PROD=hypothetical protein FLJ20950 /DB_XREF=gi:13376436 /UG=Hs.285673 hypothetical protein FLJ20950 /FL=gb:NM_024952.1
204158_s_at	gb:NM_006019.1 /DEF=Homo sapiens T-cell, immune regulator 1 (TCIRG1), mRNA. /FEA=mrna /GEN=TCIRG1 /PROD=ATPase, H+ transporting, 116kd /DB_XREF=gi:5174620 /UG=Hs.46465 T-cell, immune regulator 1 /FL=gb:U45285.1 gb:NM_006019.1
208842_s_at	Consensus includes gb:W93787 /FEA=EST /DB_XREF=gi:1422930 /DB_XREF=est:zd96c09.s1 /CLONE=IMAGE:357328 /UG=Hs.6880 DRFZF434D156 protein /FL=gb:BC001408.1
203047_at	gb:NM_005990.1 /DEF=Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /FEA=mrna /GEN=STK10 /PROD=serine/threonine kinase 10 /DB_XREF=gi:5174700 /UG=Hs.16134 serine/threonine kinase 10 /FL=gb:AB015718.1 gb:NM_005990.1 gb:AF119894.1
213408_s_at	Consensus includes gb:AK024034.1 /DEF=Homo sapiens cDNA FLJ13972 fis, clone V79A1001548, highly similar to PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67). /FEA=mrna /DB_XREF=gi:10436297 /UG=Hs.171625 phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
209858_x_at	gb:BC002877.1 /DEF=Homo sapiens, similar to hypothetical protein FLJ11585, clone MGC:11258, mRNA, complete cds. /FEA=mrna /PROD=similar to hypothetical protein FLJ11585 /DB_XREF=gi:12804048 /UG=Hs.315367 Homo sapiens, similar to hypothetical protein FLJ11585, clone MGC:11258, mRNA, complete cds /FL=gb:BC002877.1
35626_at	Cluster Incl. U30894:Human N-sulphoglucosamine sulphonyltransferase mRNA, complete cds /cds=(12,1520) /gb=U30894 /gi=1173542 /ug=Hs.31074 /len=2657
201871_s_at	gb:NM_015853.1 /DEF=Homo sapiens ORF (LOC51035), mRNA. /FEA=mrna /GEN=LOC51035 /PROD=unknown protein LOC51035 /DB_XREF=gi:7705653 /UG=Hs.77868 ORF /FL=gb:BC000902.1 gb:M68864.1 gb:NM_015853.1
212204_at	Consensus includes gb:AL049944.1 /DEF=Homo sapiens mRNA: cDNA DKF2564G2022 (from clone DKF2564G2022); partial cds. /FEA=mrna /GEN=DKF2564G2022 /PROD=hypothetical protein /DB_XREF=gi:4884189 /UG=Hs.16492 DKF2564G2022 protein
217802_s_at	gb:NM_022731.1 /DEF=Homo sapiens similar to rat nuclear ubiquitously casein kinase 2 (NUCKS), mRNA. /FEA=mrna /GEN=NUCKS /PROD=similar to rat nuclear ubiquitously casein kinase2 /DB_XREF=gi:12232386 /UG=Hs.118064 similar to rat nuclear ubiquitously casein kinase 2 /FL=gb:NM_022731.1 gb:BC000805.1
201960_s_at	gb:NM_015057.1 /DEF=Homo sapiens KIAA0916 protein (KIAA0916), mRNA. /FEA=mrna /GEN=KIAA0916 /PROD=KIAA0916 protein /DB_XREF=gi:7662379 /UG=Hs.151411 KIAA0916 protein /FL=gb:AF075587.1 gb:AF083244.1 gb:NM_015057.1
47608_at	Cluster Incl. AF697401:tlq18h09.x1 Homo sapiens cDNA, 3' end /clone=IMAGE:2209217 /clone_end=3 /gb=AF697401 /gi=4985301 /ug=Hs.9741 /len=639
210250_x_at	gb:AF067854.1 /DEF=Homo sapiens adenylosuccinate lyase (ADSL), alternatively spliced, complete cds. /FEA=mrna /GEN=ADSL /PROD=adenylosuccinate lyase /DB_XREF=gi:3211983 /UG=Hs.75527 adenylosuccinate lyase /FL=gb:AF067854.1
218495_at	gb:NM_004182.1 /DEF=Homo sapiens ubiquitously-expressed transcript (UNT), mRNA. /FEA=mrna /GEN=UNT /PROD=ubiquitously-expressed transcript /DB_XREF=gi:4759297 /UG=Hs.172791 ubiquitously-expressed transcript /FL=gb:BC000720.1 gb:AF092737.1 gb:NM_004182.1 gb:AF083241.1 gb:AF083242.1

201106_at	gb:NM_002085.1 /DEF=Homo sapiens glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), mRNA. /FEA=mrna /GEN=GPX4 / PROD=glutathione peroxidase 4 /DB_XREF=gi:4504106 /UG=Hs.2706 glutathione peroxidase 4 (phospholipid hydroperoxidase) / FL=gb:NM_002085.1
203569_s_at	gb:NM_003611.1 /DEF=Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA. /FEA=mrna /GEN=CXORF5 / PROD=chromosome X open reading frame 5 /DB_XREF=gi:4503178 /UG=Hs.6483 oral-facial-digital syndrome 1 gene /FL=gb:NM_003611.1
201316_at	Consensus includes gb:AL523904 /FEA=EST /DB_XREF=gi:12787397 /DB_XREF=est:AL523904 /CLONE=CS00C003YB07 (3 prime) / UG=Hs.181309 proteasome (prosome, macropain) subunit, alpha type, 2 /FL=gb:NM_002787.1
218336_at	gb:NM_012394.2 /DEF=Homo sapiens prefoldin 2 (PFND2), mRNA. /FEA=mrna /GEN=PFND2 /PROD=prefoldin 2 /DB_XREF=gi:12408674 / UG=Hs.298229 prefoldin 2 /FL=gb:NM_012394.2 gb:AF165883.1 gb:AF117237.1 gb:AF151085.1
209370_s_at	Consensus includes gb:BE502377 /FEA=EST /DB_XREF=gi:9704785 /DB_XREF=est:hy22g03.x1 /CLONE=IMAGE:3198100 /UG=Hs.167679 SH3-domain binding protein 2 /FL=gb:AB000462.1 gb:AF000936.1
201036_s_at	gb:NM_005327.1 /DEF=Homo sapiens L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA. /FEA=mrna /GEN=HADHSC / PROD=L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /DB_XREF=gi:4885386 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1
208776_at	Consensus includes gb:BF432873 /FEA=EST /DB_XREF=gi:11445036 /DB_XREF=est:n28a02.x1 /CLONE=IMAGE:3565730 /UG=Hs.90744 proteasome (prosome, macropain) 26S subunit, non-ATPase, 1L /FL=gb:BC000437.1 gb:BC004430.1 gb:AB003102.1 gb:AF001212.1 gb:NM_002815.1
214765_s_at	Consensus includes gb:AK024677.1 /DEF=Homo sapiens cDNA: FLJ21024 fls, clone CAE06651, highly similar to HUMPUT Human LTR RNA. / FEA=mrna /DB_XREF=gi:10437016 /UG=Hs.264330 N-acylsphingosine amidohydrolase (acid ceramidase)-like
204225_at	gb:NM_006037.2 /DEF=Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /FEA=mrna /GEN=HDAC4 /PROD=histone deacetylase 4 / DB_XREF=gi:13259519 /UG=Hs.91400 histone deacetylase 4 /FL=gb:NM_006037.2 gb:AF132607.1
214170_x_at	Consensus includes gb:AA669797 /FEA=EST /DB_XREF=gi:2631296 /DB_XREF=est:ag36c01.s1 /CLONE=IMAGE:1118880 /UG=Hs.75653 fumarate hydratase
218210_at	gb:NM_024619.1 /DEF=Homo sapiens hypothetical protein FLJ12171 (FLJ12171), mRNA. /FEA=mrna /GEN=FLJ12171 /PROD=hypothetical protein FLJ12171 /DB_XREF=gi:13375839 /UG=Hs.31431 hypothetical protein FLJ12171 /FL=gb:AL336631.1 gb:NM_024619.1
218652_s_at	gb:NM_017733.1 /DEF=Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /FEA=mrna /GEN=FLJ20265 /PROD=hypothetical protein FLJ20265 /DB_XREF=gi:8923239 /UG=Hs.7099 hypothetical protein FLJ20265 /FL=gb:BC001249.1 gb:BC000937.2 gb:NM_017733.1
201270_x_at	gb:NM_015332.1 /DEF=Homo sapiens KIAA1068 protein (KIAA1068), mRNA. /FEA=mrna /GEN=KIAA1068 /PROD=KIAA1068 protein / DB_XREF=gi:13357209 /UG=Hs.4770 KIAA1068 protein /FL=gb:BC003691.1 gb:NM_015332.1
203906_at	Consensus includes gb:AT652645 /FEA=EST /DB_XREF=gi:4736624 /DB_XREF=est:wb30b07.x1 /CLONE=IMAGE:2307157 /UG=Hs.4764 KIAA0763 gene product /FL=gb:AB018306.1 gb:NM_014869.1
221516_s_at	gb:BC002587.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:1067, mRNA, complete cds. /FEA=mrna /PROD=hypothetical protein / DB_XREF=gi:12803520 /UG=Hs.83869 hypothetical protein /FL=gb:BC002587.1
209492_x_at	gb:BC003679.1 /DEF=Homo sapiens, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e, clone MGC:12532, mRNA, complete cds. /FEA=mrna /PROD=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e /DB_XREF=gi:13277543 / UG=Hs.85539 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e /FL=gb:BC003679.1
212048_s_at	Consensus includes gb:AW245400 /FEA=EST /DB_XREF=gi:6588393 /DB_XREF=est:2822751.3prime /CLONE=IMAGE:2822751 /UG=Hs.239307 tyrosyl-tRNA synthetase
204214_s_at	gb:NM_006834.1 /DEF=Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA. /FEA=mrna /GEN=RAB32 /PROD=RAB32, member oncogene family /DB_XREF=gi:5803132 /UG=Hs.32217 RAB32, member RAS oncogene family /FL=gb:U71127.1 gb:NM_006834.1
217796_s_at	gb:NM_017921.1 /DEF=Homo sapiens hypothetical protein FLJ20657 (FLJ20657), mRNA. /FEA=mrna /GEN=FLJ20657 /PROD=hypothetical protein FLJ20657 /DB_XREF=gi:89232608 /UG=Hs.164256 hypothetical protein FLJ20657 /FL=gb:NM_017921.1
203327_at	Consensus includes gb:N22903 /FEA=EST /DB_XREF=gi:1137053 /DB_XREF=est:yx66e04.s1 /CLONE=IMAGE:266718 /UG=Hs.1508 insulin-degrading enzyme /FL=gb:M21188.1 gb:NM_004969.1
208659_at	gb:AF034607.1 /DEF=Homo sapiens chloride channel ABP mRNA, complete cds. /FEA=mrna /PROD=chloride channel ABP /DB_XREF=gi:4426566 / UG=Hs.74276 chloride intracellular channel 1 /FL=gb:U93205.1 gb:AF034607.1 gb:AF109197.1 gb:NM_001288.2
222218_s_at	Consensus includes gb:AJ400843.1 /DEF=Homo sapiens partial mRNA for immunoglobulin-like cell surface receptor FDF03-M14, soluble alternative form. /FEA=mrna /GEN=FDF03-M14 /PROD=cell surface receptor FDF03-M14 /DB_XREF=gi:9715838 /UG=Hs.122591 paired immunoglobulin-like receptor alpha
211862_x_at	gb:AF015451.1 /DEF=Homo sapiens Usurpin-beta mRNA, complete cds. /FEA=CDS /PROD=Usurpin-beta /DB_XREF=gi:3133282 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:AF015451.1

209080_x_at	gb:AF118652.1 / DEF=Homo sapiens PKC-interacting protein PICOT (PICOT) mRNA, complete cds. / FEA-mRNA / GEN=PICOT / PROD=PKC-interacting protein PICOT / DB_XREF=gi:6840952 / UG=Hs.42644 thiorodoxin-like / FL=gb:BC005289.1 gb:AF118649.1 gb:AF118652.1
209789_at	gb:NM_001398.1 / DEF=Homo sapiens enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA. / FEA-mRNA / GEN=ECH1 / PROD=peroxisomal enoyl-coenzyme A hydratase-like protein / DB_XREF=gi:4503446 / UG=Hs.196176 enoyl Coenzyme A hydratase 1, peroxisomal / FL=gb:NM_001398.1 gb:U16660.1
90610_at	Cluster Incl. AI654857:wb45b10.x1 Homo sapiens cDNA, 3' end / clone=IMAGE-2310523 / clone_end=3 / gb=AI654857 / gi=4738836 / UG=Hs.160115 / len=621
201704_at	gb:NM_001247.1 / DEF=Homo sapiens ectonucleoside triphosphate diphosphohydrolase 6 (putative function) (ENTPD6), mRNA. / FEA-mRNA / GEN=ENTPD6 / PROD=ectonucleoside triphosphate diphosphohydrolase 6 (putative function) / DB_XREF=gi:4557422 / UG=Hs.12330 ectonucleoside triphosphate diphosphohydrolase 6 (putative function) / FL=gb:AF039916.1 gb:NM_001247.1
218026_at	gb:NM_014019.1 / DEF=Homo sapiens HSPC009 protein (HSPC009), mRNA. / FEA-mRNA / GEN=HSPC009 / PROD=HSPC009 protein / DB_XREF=gi:7661731 / UG=Hs.16059 HSPC009 protein / FL=gb:BC002698.1 gb:AF070665.1 gb:NM_014019.1
214771_x_at	Consensus includes gb:AK025604.1 / DEF=Homo sapiens cDNA: FLJ21951 fls, clone HEP04968. / FEA-mRNA / DB_XREF=gi:10438172 / UG=Hs.84883 KIAA0864 protein
208760_at	Consensus includes gb:AL031714 / DEF=Human DNA sequence from clone LA16-358B7 on chromosome 16 Contains the UBE21 gene for ubiquitin-conjugating enzyme E21 (homologous to yeast UBC9), and an RPS20 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSs, GSSs and a putative CpG is... / FEA-mRNA / DB_XREF=gi:4775608 / UG=Hs.84285 ubiquitin-conjugating enzyme E21 (homologous to yeast UBC9) / FL=gb:U45328.1 gb:U31933.1 gb:BC000427.1 gb:BC004429.1 gb:U31882.1 gb:U66867.1 gb:U38785.1 gb:NM_003345.1 gb:U29092.1
212607_at	Consensus includes gb:N32526 / FEA=EST / DB_XREF=gi:1152925 / DB_XREF=est:yy11f04.s1 / CLONE=IMAGE:270943 / UG=Hs.300642 serologically defined colon cancer antigen 8
64418_at	Cluster Incl. AI472320:tj87c02.x1 Homo sapiens cDNA, 3' end / clone=IMAGE-2148482 / clone_end=3 / gb=AI472320 / gi=4334410 / UG=Hs.48504 / len=548
205819_at	gb:NM_006770.1 / DEF=Homo sapiens macrophage receptor with collagenous structure (MARCO), mRNA. / FEA-mRNA / GEN=MARCO / PROD=macrophage receptor with collagenous structure / DB_XREF=gi:5803079 / UG=Hs.67726 macrophage receptor with collagenous structure / FL=gb:AF035819.1 gb:NM_006770.1
218019_s_at	gb:NM_021941.1 / DEF=Homo sapiens hypothetical protein FLJ21324 (FLJ21324), mRNA. / FEA-mRNA / GEN=FLJ21324 / PROD=hypothetical protein FLJ21324 / DB_XREF=gi:11345479 / UG=Hs.4746 hypothetical protein FLJ21324 / FL=gb:NM_021941.1 gb:BC003651.1
219220_x_at	gb:NM_020191.1 / DEF=Homo sapiens GK002 protein (GK002), mRNA. / FEA-mRNA / GEN=GK002 / PROD=GK002 protein / DB_XREF=gi:9910243 / UG=Hs.107127 GK002 protein; gbt protein; chromosome 3 open reading frame 5 / FL=gb:AF321613.1 gb:AF226045.1 gb:NM_020191.1
212355_at	Consensus includes gb:AI075450 / FEA=EST / DB_XREF=gi:3399805 / DB_XREF=est:oz82g10.x1 / CLONE=IMAGE:1681890 / UG=Hs.7911 KIAA0323 protein
214735_at	Consensus includes gb:AM166711 / FEA=EST / DB_XREF=gi:6398236 / DB_XREF=est:xg27h02.x1 / CLONE=IMAGE:2628819 / UG=Hs.185140 KIAA0403 protein
219041_s_at	gb:NM_014374.1 / DEF=Homo sapiens zinc finger protein (AP4), mRNA. / FEA-mRNA / GEN=AP4 / PROD=zinc finger protein / DB_XREF=gi:7656889 / UG=Hs.90693 zinc finger protein / FL=gb:BC000363.1 gb:NM_014374.1
209110_s_at	gb:AL050259.1 / DEF=Homo sapiens mRNA; cDNA DKF2564D0782 (from clone DKF2564D0782); complete cds. / FEA-mRNA / GEN=DKF2564D0782 / PROD=hypothetical protein / DB_XREF=gi:4886476 / UG=Hs.170160 RAB2, member RAS oncogene family-like / FL=gb:D85757.1 gb:NM_004761.1 gb:AL050259.1
215691_x_at	Consensus includes gb:AV702994 / FEA=EST / DB_XREF=gi:10719324 / DB_XREF=est:AV702994 / CLONE=ADBAFP06 / UG=Hs.46967 HSPC034 protein
207614_s_at	gb:NM_003592.1 / DEF=Homo sapiens cullin 1 (CUL1), mRNA. / FEA-mRNA / GEN=CUL1 / PROD=cullin 1 / DB_XREF=gi:4503160 / UG=Hs.14541 cullin 1 / FL=gb:U58087.1 gb:NM_003592.1
213405_at	Consensus includes gb:N95443 / FEA=EST / DB_XREF=gi:1267753 / DB_XREF=est:zb81c12.s1 / CLONE=IMAGE:310006 / UG=Hs.19180 Homo sapiens mRNA; cDNA DKF2564E122 (from clone DKF2564E122)
208835_s_at	Consensus includes gb:AW089673 / FEA=EST / DB_XREF=gi:6047017 / DB_XREF=est:xc21h11.x1 / CLONE=IMAGE:2594469 / UG=Hs.3688 cisplatin resistance-associated overexpressed protein / FL=gb:AB034405.1
202225_at	Consensus includes gb:AW612311 / FEA=EST / DB_XREF=gi:7317497 / DB_XREF=est:hg95e07.x1 / CLONE=IMAGE:2953380 / UG=Hs.306088 v-crk avian sarcoma virus CT10 oncogene homolog / FL=gb:D10656.1 gb:NM_016823.1
218358_at	gb:NM_024324.1 / DEF=Homo sapiens hypothetical protein MGCL1256 (MGCL1256), mRNA. / FEA-mRNA / GEN=MGCL1256 / PROD=hypothetical protein

	MGC11256 /DB_XREF=gi:13236568 /UG=Hs.28029 hypothetical protein MGC11256 /FL=gb:BC002894.1 gb:Nm_024324.1
213511_s_at	Consensus includes gb:A1167164 /FEA=EST./DB_XREF=gi:3700334 /DB_XREF=est:oo08c10.x1 /CLONE=IMAGE:1565586 /UG=Hs.23200 myotubularin related protein 1
218133_s_at	gb:Nm_021824.1 /DEF=Homo sapiens NTF3 [Ngg1 interacting factor 3, S.pombe homolog]-like 1 (NTF3L1), mRNA. /FEA=mRNA /GEN=NTPF3L1 /PROD=NIF3 [Ngg1 interacting factor 3, S.pombehomolog]-like 1 /FE=gb:AF182416.1 gb:Nm_021824.1 gb:AF060513.1 gb:AB038949.1
218133_s_at	S.pombe homolog)-like 1 /FL=gb:AF182416.1 gb:Nm_021824.1 gb:AF060513.1 gb:AB038949.1
	Consensus includes gb:AI297512 /FEA=EST /DB_XREF=gi:5663476 /DB_XREF=est:w090g11.x1 /CLONE=IMAGE:2462660 /UG=Hs.77495 UBX domain-containing 1
212007_at	gb:Nm_004853.1 /DEF=Homo sapiens syntaxin 8 (STX8), mRNA. /FEA=mRNA /GEN=STX8 /PROD=syntaxin 8 /DB_XREF=gi:4759187 /UG=Hs.119525 syntaxin 8 /FL=gb:AF062077.1 gb:AF036715.1 gb:AF115323.1 gb:Nm_004853.1
204690_at	gb:AF073890.1 /DEF=Homo sapiens cathepsin X precursor, mRNA, complete cds. /FEA=mRNA /PROD=cathepsin X precursor /DB_XREF=gi:3650497 /UG=Hs.252349 cathepsin Z /FL=gb:AF032906.1 gb:AF073890.1 gb:Nm_001336.1 gb:AF136273.1
210042_s_at	Cluster Incl. AB007915:Homo sapiens mRNA for KIAA0446 protein, complete cds /cds=(3531,4286) /gb=AB007915 /gi=3413853 /ug=Hs.158286 /len=6944
32091_at	gb:Nm_004092.2 /DEF=Homo sapiens enoyl Coenzyme A hydratase, short chain, 1; mitochondrial (ECHS1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ECHS1 /PROD=mitochondrial short-chain enoyl-Coenzyme A hydratase 1 precursor /DB_XREF=gi:12707569 /UG=Hs.76394 enoyl Coenzyme A hydratase, short chain, 1, mitochondrial /FL=gb:Nm_004092.2 gb:DL3900.1
201135_at	gb:Nm_017971.1 /DEF=Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA. /FEA=mRNA /GEN=FLJ10024 /PROD=hypothetical protein FLJ10024 /DB_XREF=gi:8922189 /UG=Hs.182698 hypothetical protein FLJ10024 /FL=gb:Nm_017971.1
220526_s_at	gb:Nm_002198.1 /DEF=Homo sapiens interferon regulatory factor 1 (IRF1), mRNA. /FEA=mRNA /GEN=IRF1 /PROD=interferon regulatory factor 1 /DB_XREF=gi:4504720 /UG=Hs.80645 interferon regulatory factor 1 /FL=gb:Nm_002198.1
202531_at	Consensus includes gb:BF718769 /FEA=EST /DB_XREF=gi:12019514 /DB_XREF=est:KES772 /CLONE=S90413.NIH-107-R.ab1 /UG=Hs.36587 protein phosphatase 1, regulatory subunit 7
213465_s_at	gb:Nm_001607.2 /DEF=Homo sapiens acetyl-Coenzyme A acyltransferase 1 (peroxisomal)-Coenzyme A thiolase (ACAA1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACAA1 /PROD=acetyl-Coenzyme A acyltransferase 1 /DB_XREF=gi:6598316 /UG=Hs.166160 acetyl-Coenzyme A acyltransferase 1 (peroxisomal)-Coenzyme A thiolase /FL=gb:BC000635.1 gb:Nm_001607.2
202025_x_at	gb:Nm_007049.1 /DEF=Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA. /FEA=mRNA /GEN=BTN2A1 /PROD=butyrophilin, subfamily 2, member A1 /DB_XREF=gi:5921460 /UG=Hs.169963 butyrophilin, subfamily 2, member A1 /FL=gb:U90543.1 gb:Nm_007049.1
203944_x_at	Consensus includes gb:A131324 /FEA=EST /DB_XREF=gi:4018929 /DB_XREF=est:ta77f02.x2 /CLONE=IMAGE:2050107 /UG=Hs.795 H2A histone family, member O
214290_s_at	gb:Nm_005537.1 /DEF=Homo sapiens inhibitor of growth 1 family, member 1 (ING1), mRNA. /FEA=mRNA /GEN=ING1 /PROD=inhibitor of growth 1 family, member 1 /DB_XREF=gi:5031792 /UG=Hs.46700 inhibitor of growth 1 family, member 1 /FL=gb:AF001954.1 gb:Nm_005537.1
208415_x_at	Consensus includes gb:AF131850.1 /DEF=Homo sapiens clone 24988 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406694 /UG=Hs.286027 etoposide-induced mRNA
216396_s_at	gb:Nm_000143.1 /DEF=Homo sapiens fumarate hydratase (FH), mRNA. /FEA=mRNA /GEN=FH /PROD=fumarate hydratase /DB_XREF=gi:4503716 /UG=Hs.75653 fumarate hydratase /FL=gb:BC003108.1 gb:M15502.1 gb:U99309.1 gb:U48857.1 gb:Nm_000143.1
203033_x_at	gb:Nm_001839.1 /DEF=Homo sapiens solute carrier family 31 (copper transporters), member 1 (SLC31A1), mRNA. /FEA=mRNA /GEN=SLC31A1 /PROD=solute carrier family 31 (copper transporters), member 1 /DB_XREF=gi:4507014 /UG=Hs.73614 solute carrier family 31 (copper transporters); member 1 /FL=gb:U83460.1 gb:Nm_001839.1
203971_at	gb:Nm_003369.1 /DEF=Homo sapiens UV radiation resistance associated gene (UVRAG), mRNA. /FEA=mRNA /GEN=UVRAG /PROD=UV radiation resistance associated gene /DB_XREF=gi:4507860 /UG=Hs.13137 UV radiation resistance associated gene /FL=gb:Nm_003369.1 gb:AB012958.1
203241_at	translational initiation factor 2, subunit 1 (alpha, 35kd) /FL=gb:BC002513.1 gb:UC02645.1 gb:Nm_004094.1
201142_at	Consensus includes gb:AA577698 /FEA=EST /DB_XREF=gi:12355882 /DB_XREF=est:m22n05.s1 /CLONE=IMAGE:1084665 /UG=Hs.151777 eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd)
208818_s_at	PROD=catechol-O-methyltransferase /DB_XREF=gi:12653300 /UG=Hs.240013 catechol-O-methyltransferase /FL=gb:EC000419.1 gb:M58525.1
203436_at	gb:Nm_006413.1 /DEF=Homo sapiens ribonuclease P (30KD) (RPP30), mRNA. /FEA=mRNA /GEN=RPP30 /PROD=ribonuclease P (30KD) /DB_XREF=gi:5454023 /UG=Hs.139120 ribonuclease P (30KD) /FL=gb:U77665.1 gb:Nm_006413.1

201380_at	gb:NM_006371.1 /DEF=Homo sapiens cartilage associated protein (CRTAP), mRNA. /FEA=mrna /GEN=CRTAP /PROD=cartilage associated protein /DB_XREF=gi:5453600 /UG=Hs.155481 cartilage associated protein /FL=gb:NM_006371.1
203614_at	gb:NM_021645.1 /DEF=Homo sapiens KIAA0266 gene product (KIAA0266), mRNA. /FEA=mrna /GEN=KIAA0266 /PROD=KIAA0266 gene product /DB_XREF=gi:11063982 /UG=Hs.127376 KIAA0266 gene product /FL=gb:NM_021645.1 gb:D87455.1
208649_s_at	gb:AF100752.1 /DEF=Homo sapiens transitional endoplasmic reticulum ATPase mRNA, complete cds. /FEA=mrna /PROD=transitional endoplasmic reticulum ATPase /DB_XREF=gi:5410289 /UG=Hs.106357 valosin-containing protein /FL=gb:AF100752.1 gb:NM_007126.2
209012_at	Consensus includes gb:AV718192 /FEA=EST /DB_XREF=gi:10815344 /DB_XREF=est:AV718192 /CLONE=PHYABE08 /UG=Hs.171957 triple functional domain (PTPRF interacting) /FL=gb:AF091395.1
212100_s_at	Consensus includes gb:293241 /DEF=Human DNA sequence from clone 22E13 on chromosome 22. Contains three novel genes, an ATP Synthase G Chain, Mitochondrial (EC 3.6.3.34) pseudogene and the DIAL gene for diaphorase (NADH) (cytochrome b-5 reductase) (EC 1.6.2.2). Contains ESTs, STSs, ... /FEA=mrna 5 /DB_XREF=gi:4826450 /UG=Hs.278314 hypothetical protein
208756_at	gb:U36764.1 /DEF=Human TGF-beta receptor interacting protein 1 mRNA, complete cds. /FEA=mrna /PROD=TGF-beta receptor interacting protein 1 /DB_XREF=gi:1036804 /UG=Hs.192023 eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) /FL=gb:U36764.1
213034_at	gb:BC000413.1 gb:BC003140.1 gb:U39067.1 gb:NM_003757.1 gb:AF116697.1
200684_s_at	Consensus includes gb:AB023216.1 /DEF=Homo sapiens mRNA for KIAA0999 protein, partial cds. /FEA=mrna /GEN=KIAA0999 /PROD=KIAA0999 protein /DB_XREF=gi:4589641 /UG=Hs.4278 KIAA0999 protein
213019_at	Consensus includes gb:AF1819709 /FEA=EST /DB_XREF=gi:5438788 /DB_XREF=est:wj77c07.x1 /CLONE=IMAGE:2408844 /UG=Hs.108104 ubiquitin-conjugating enzyme E2L 3 /FL=gb:NM_003347.1
218617_at	Consensus includes gb:AF112233 /FEA=EST /DB_XREF=gi:3538999 /DB_XREF=est:qa47e04.x1 /CLONE=IMAGE:1689918 /UG=Hs.167496 RAN binding protein 6
208308_s_at	gb:NM_017646.1 /DEF=Homo sapiens tRNA-isopentenylpyrophosphate transferase (IPT), mRNA. /FEA=mrna /GEN=IPT /PROD=tRNA isopentenylpyrophosphate transferase /DB_XREF=gi:8923064 /UG=Hs.288036 tRNA isopentenylpyrophosphate transferase /FL=gb:NM_017646.1
209429_x_at	gb:NM_000175.1 /DEF=Homo sapiens glucose phosphate isomerase (GPI), mRNA. /FEA=mrna /GEN=GPI /PROD=glucose phosphate isomerase /DB_XREF=gi:4504086 /UG=Hs.180532 glucose phosphate isomerase /FL=gb:BC004982.1 gb:K03515.1 gb:NM_000175.1
221501_x_at	gb:AF112207.1 /DEF=Homo sapiens translation initiation factor eIF-2b subunit mRNA, complete cds. /FEA=mrna /PROD=translation initiation factor eIF-2b subunit /DB_XREF=gi:6563201 /UG=Hs.169474 DKFZP586U0119 protein /FL=gb:BC001870.1 gb:AF112207.1
209161_at	gb:AF229069.1 /DEF=Homo sapiens KIAA0220-like protein mRNA, complete cds. /FEA=mrna /PROD=KIAA0220-like protein /DB_XREF=gi:8980670 /UG=Hs.251928 nuclear pore complex interacting protein /FL=gb:AF229069.1
201414_s_at	Consensus includes gb:AF184802 /FEA=EST /DB_XREF=gi:3735440 /DB_XREF=est:qd24g04.x1 /CLONE=IMAGE:1724694 /UG=Hs.8551 PRP4STKWD splicing factor /FL=gb:AF016369.1 gb:U82756.1 gb:NM_004697.1
212361_s_at	gb:NM_005969.1 /DEF=Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA. /FEA=mrna /GEN=NAP1L4 /PROD=nucleosome assembly protein 1-like 4 /DB_XREF=gi:5174612 /UG=Hs.78103 nucleosome assembly protein 1-like 4 /FL=gb:U77456.1 gb:NM_005969.1
204084_s_at	Consensus includes gb:AW190070 /FEA=EST /DB_XREF=gi:6464550 /DB_XREF=est:x111f11.x1 /CLONE=IMAGE:2675949 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
203200_s_at	Consensus includes gb:AF1911687 /FEA=EST /DB_XREF=gi:5631542 /DB_XREF=est:wc71g01.x1 /CLONE=IMAGE:2324112 /UG=Hs.30213 ceroid-lipofuscinosis, neuronal 5 /FL=gb:AF068227.1 gb:NM_006493.1
201405_s_at	gb:NM_024010.1 /DEF=Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 2, mRNA. /FEA=mrna /GEN=MTRR /PROD=methionine synthase reductase, isoform 2 /DB_XREF=gi:13325067 /UG=Hs.153792 5-methyltetrahydrofolate-homocysteine methyltransferase reductase /FL=gb:NM_024010.1 gb:AF121214.1
218556_at	gb:NM_006833.1 /DEF=Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (MOV34-34kD), mRNA. /FEA=mrna /GEN=MOV34-34kD /PROD=COP9 subunit 6 (MOV34 homolog, 34 kD) /DB_XREF=gi:5803095 /UG=Hs.15591 COP9 subunit 6 (MOV34 homolog, 34 kD) /FL=gb:BC002520.1 gb:U70735.1 gb:NM_006833.1
217756_x_at	gb:NM_014182.1 /DEF=Homo sapiens HSPC160 protein (HSPC160), mRNA. /FEA=mrna /GEN=HSPC160 /PROD=HSPC160 protein /DB_XREF=gi:7661819 /UG=Hs.13144 HSPC160 protein /FL=gb:AF161509.1 gb:NM_014182.1
	gb:NM_005770.1 /DEF=Homo sapiens small EDRK-rich factor 2 (SERP2), mRNA. /FEA=mrna /GEN=SERP2 /PROD=small EDRK-rich factor 2 /DB_XREF=gi:5032084 /UG=Hs.323806 small EDRK-rich factor 2 /FL=gb:AF320073.1 gb:AF073298.1 gb:NM_005770.1



209206_at	Consensus includes gb:AV701283 /FEA=EST /DB_XREF=gi:10717613 /DB_XREF=est:AV701283 /CLONE=ADAGD06 /UG=Hs.50785 SEC22; vesicle trafficking protein (S. cerevisiae)-like 1 /FL=gb:BC001364.1 gb:AF047442.1 gb:NM_004892.1
212165_at	Consensus includes gb:AF070537.1 /DEF=Homo sapiens clone 24606 mRNA sequence. /FEA=mrna /DB_XREF=gi:3387894 /UG=Hs.17481 Homo sapiens clone 24606 mRNA sequence
208983_s_at	gb:M37780.1 /DEF=Human leukocyte surface protein (CD31) mRNA, complete cds. /FEA=mrna /GEN=CD31 /PROD=leukocyte surface protein /DB_XREF=gi:1187239 /UG=Hs.78146 plateletendothelial cell adhesion molecule (CD31 antigen) /FL=gb:M37780.1 gb:M8526.1 gb:NM_000442.1
202042_at	gb:NM_002109.2 /DEF=Homo sapiens histidyl-CRNA synthetase (HARS), mRNA. /FEA=mrna /GEN=HARS /PROD=histidyl tRNA synthetase /DB_XREF=gi:6996013 /UG=Hs.77798 histidyl-tRNA synthetase /FL=gb:NM_002109.2
202433_at	gb:NM_005827.1 /DEF=Homo sapiens UDP-galactose transporter related (UGTREL1), mRNA. /FEA=mrna /GEN=UGTREL1 /PROD=UDP-galactose transporter related /DB_XREF=gi:5032212 /UG=Hs.154073 UDP-galactose transporter related /FL=gb:D87989.1
201145_at	gb:NM_005827.1 /DEF=Homo sapiens HSI binding protein (HAX1), mRNA. /FEA=mrna /GEN=HAX1 /PROD=HSI binding protein /DB_XREF=gi:1343535 /UG=Hs.15318 HSI binding protein /FL=gb:NM_006118.2 gb:BC005240.1 gb:U68566.1
211975_at	Consensus includes gb:BE299671 /FEA=EST /DB_XREF=gi:9103419 /DB_XREF=est:60094434T1 /CLONE=IMAGE:2960218 /UG=Hs.256310 protein kinase C and casein kinase substrate in neurons 3
200918_s_at	gb:NM_003139.1 /DEF=Homo sapiens signal recognition particle receptor (docking protein) (SRPR), mRNA. /FEA=mrna /GEN=SRPR /PROD=signal recognition particle receptor (docking protein) /DB_XREF=gi:4507222 /UG=Hs.75730 signal recognition particle receptor (docking protein) /FL=gb:BC001162.1 gb:NM_003139.1
203497_at	gb:NM_004774.1 /DEF=Homo sapiens PPAR binding protein (PPARBP), mRNA. /FEA=mrna /GEN=PPARBP /PROD=thyroid hormone receptor interactor 2 /DB_XREF=gi:4759265 /UG=Hs.15589 PPAR binding protein /FL=gb:AF055994.1 gb:NM_004774.1 gb:AF283812.1
209153_s_at	gb:M31523.1 /DEF=Human transcription factor (E2A) mRNA, complete cds. /FEA=mrna /GEN=TCF3 /DB_XREF=gi:339477 /UG=Hs.101047 transcription factor 3 (E2A immunoglobulin enhancer binding factors E12B47) /FL=gb:M31523.1
220966_x_at	gb:NM_030978.1 /DEF=Homo sapiens hypothetical protein similar to actin related protein 23 complex, subunit 5 (MGC3038), mRNA. /FEA=mrna /GEN=MGC3038 /PROD=hypothetical protein similar to actin related protein 23 complex, subunit 5 /DB_XREF=gi:1356995 /FL=gb:NM_030978.1
212785_s_at	Consensus includes gb:AA160181 /FEA=EST /DB_XREF=gi:1734757 /DB_XREF=est:z081d09.s1 /CLONE=IMAGE:593297 /UG=Hs.278635 HDCMA18P protein
219176_at	gb:NM_024520.1 /DEF=Homo sapiens hypothetical protein FLJ22555 (FLJ22555), mRNA. /FEA=mrna /GEN=FLJ22555 /PROD=hypothetical protein FLJ22555 /DB_XREF=gi:13375659 /UG=Hs.3592 hypothetical protein FLJ22555 /FL=gb:NM_024520.1
218679_s_at	gb:NM_016208.1 /DEF=Homo sapiens VPS28 protein (LOC51160), mRNA. /FEA=mrna /GEN=LOC51160 /PROD=VPS28 protein /DB_XREF=gi:7705884 /UG=Hs.293441 VPS28 protein /FL=gb:AF316887.1 gb:AF182844.1 gb:NM_016208.1
206991_s_at	gb:NM_000579.1 /DEF=Homo sapiens chemokine (C-C motif) receptor 5 (CCR5), mRNA. /FEA=mrna /GEN=CCR5 /PROD=chemokine (C-C motif) receptor 5 /DB_XREF=gi:4502638 /UG=Hs.54443 chemokine (C-C motif) receptor 5 /FL=gb:U54994.1 gb:U57840.1 gb:NM_000579.1
209770_at	gb:U90552.1 /DEF=Human butyrophilin (BTF5) mRNA, complete cds. /FEA=mrna /GEN=BTF5 /PROD=butyrophilin /DB_XREF=gi:2062705 /UG=Hs.284283 butyrophilin, subfamily 3, member A1 /FL=gb:U90552.1
214268_s_at	Consensus includes gb:AL042220 /FEA=EST /DB_XREF=gi:5421564 /DB_XREF=est:DKFZp434H1920.s1 /CLONE=DKFZp434H1920 /UG=Hs.141727 myotubularin related protein 4
201885_s_at	gb:NM_000398.3 /DEF=Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIAL), nuclear gene encoding mitochondrial protein, transcript variant M, mRNA. /FEA=mrna /GEN=DIAL /PROD=cytochrome b5 reductase, membrane-bound isoform /DB_XREF=gi:6552326 /UG=Hs.274464 diaphorase (NADH) (cytochrome b-5 reductase) /FL=gb:BC004821.1 gb:NM_000398.3
209688_s_at	gb:BC005078.1 /DEF=Homo sapiens, clone MGC:13033, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:13033) /DB_XREF=gi:13477224 /UG=Hs.26118 Homo sapiens clone 24766 mRNA sequence /FL=gb:BC005078.1
203487_s_at	gb:NM_015396.1 /DEF=Homo sapiens DKFZP434A043 protein (DKFZP434A043), mRNA. /FEA=mrna /GEN=DKFZP434A043 /PROD=DKFZP434A043 protein /DB_XREF=gi:13477224 /UG=Hs.102708 DKFZP434A043 protein (FL=gb:NM_015396.1
202155_s_at	gb:NM_005085.1 /DEF=Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA. /FEA=mrna /GEN=NUP214 /PROD=nucleoporin 214kD (CAIN) /DB_XREF=gi:4826873 /UG=Hs.170285 nucleoporin 214kD (CAIN) /FL=gb:NM_005085.1
221786_at	Consensus includes gb:BF197222 /FEA=EST /DB_XREF=gi:11085906 /DB_XREF=est:7m88b07.x1 /CLONE=IMAGE:3561949 /UG=Hs.12342 Homo sapiens Clone 24538 mRNA sequence
212846_at	Consensus includes gb:AA811192 /FEA=EST /DB_XREF=gi:2880803 /DB_XREF=est:ob72b08.s1 /CLONE=IMAGE:1336887 /UG=Hs.152629 KIAA0179 protein



209444_at	gb:BC001851.1 /DEF=Homo sapiens, similar to RAP1, GTP-GDP dissociation stimulator 1, clone MGC:4525, mRNA, complete cds. /FEA=mrna /PROD=Similar to RAP1, GTP-GDP dissociation stimulator1 /DB_XREF=gi:12804812 /UG=Hs.7940 RAP1, GTP-GDP dissociation stimulator 1 /FL=gb:NM_021159.1 gb:BC001851.1 gb:BC001816.1 gb:AF215923.1 gb:AF237413.1
211937_at	Consensus includes gb:NM_001417.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA. /FEA=CDS /GEN=EIF4B /PROD=eukaryotic translation initiation factor 4B /DB_XREF=gi:4503532 /UG=Hs.93379 eukaryotic translation initiation factor 4B /FL=gb:NM_001417.1
201800_s_at	gb:AF185696.1 /DEF=Homo sapiens oxysterol-binding protein 1 (OSBP1) mRNA, complete cds. /FEA=mrna /GEN=OSBP1 /PROD=oxysterol-binding protein 1 /DB_XREF=gi:10441379 /UG=Hs.24734 oxysterol binding protein /FL=gb:AF185696.1 gb:M86917.1 gb:NM_002556.1
211730_s_at	gb:BC005903.1 /DEF=Homo sapiens, polymerase (RNA) II (DNA directed) polypeptide L (7.6kD), clone MGC:14494, mRNA, complete cds. /FEA=mrna /PROD=polymerase (RNA) II (DNA directed) polypeptide L(7.6kD) /DB_XREF=gi:13543491 /FL=gb:BC005903.1
65635_at	Cluster Incl. AL044097:DKF2p43M198.s1 Homo sapiens cDNA, 3 end /clone=DKF2p43M198 /clone_end=3 /gb:AL044097 /gi:5432324 /ug=Hs.29288 /len=605
207438_s_at	gb:NM_005701.1 /DEF=Homo sapiens RNA, U transporter 1 (RNUT1), mRNA. /FEA=mrna /GEN=RNUT1 /PROD=RNA, U transporter 1 /DB_XREF=gi:5031832 /UG=Hs.21577 RNA, U transporter 1 /FL=gb:AF039029.1 gb:NM_005701.1
221819_at	Consensus includes gb:BF791960 /FEA=EST /DB_XREF=gi:12097014 /DB_XREF=est:60252342F1 /CLONE=IMAGE:4344539 /UG=Hs.94308 Homo sapiens cDNA FLJ10447 fis, clone NT2RP1000851
203912_s_at	gb:NM_006730.1 /DEF=Homo sapiens deoxyribonuclease I-like 1 (DNASE1L1), mRNA. /FEA=mrna /GEN=DNASE1L1 /PROD=deoxyribonuclease I-like 1 /DB_XREF=gi:5803006 /UG=Hs.77091 deoxyribonuclease I-like 1 /FL=gb:U06846.1 gb:NM_006730.1
216996_s_at	Consensus includes gb:AK021557.1 /DEF=Homo sapiens cDNA FLJ11495 fis, clone HEMBA1001950, highly similar to Homo sapiens mRNA for KIAA0971 protein. /FEA=mrna /DB_XREF=gi:10432760 /UG=Hs.84429 KIAA0971 protein
202138_x_at	gb:NM_006303.2 /DEF=Homo sapiens JTV1 gene (JTV1), mRNA. /FEA=mrna /GEN=JTV1 /PROD=JTV1 /UG=Hs.301613 JTV1 gene /FL=gb:NM_006303.2 gb:U24169.1 gb:BC002853.1
219007_at	gb:NM_024647.1 /DEF=Homo sapiens hypothetical protein FLJ13287 (FLJ13287), mRNA. /FEA=mrna /GEN=FLJ13287 /PROD=hypothetical protein FLJ13287 /DB_XREF=gi:13375888 /UG=Hs.53263 hypothetical protein FLJ13287 /FL=gb:NM_024647.1
219714_s_at	gb:NM_018398.1 /DEF=Homo sapiens calcium channel alpha2-delta3 subunit (HSA272268), mRNA. /FEA=mrna /GEN=HSA272268 /PROD=calcium channel alpha2-delta3 subunit /DB_XREF=gi:8923764 /UG=Hs.22958 calcium channel, voltage-dependent, alpha 2delta 3 subunit /FL=gb:NM_018398.1
201263_at	gb:NM_003191.1 /DEF=Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. /FEA=mrna /GEN=TARS /PROD=threonyl-tRNA synthetase /DB_XREF=gi:4507366 /UG=Hs.84131 threonyl-tRNA synthetase /FL=gb:BC000517.1 gb:M53180.1 gb:NM_003191.1
201157_s_at	Consensus includes gb:AF020500.1 /DEF=Homo sapiens myristoyl CoA:protein N-myristoyltransferase mRNA, complete cds. /FEA=CDS /PROD=myristoyl CoA:protein N-myristoyltransferase /DB_XREF=gi:2760893 /UG=Hs.111039 N-myristoyltransferase 1 /FL=gb:NM_021079.1 gb:AF020500.1 gb:AF043324.1
221593_s_at	gb:BC001663.1 /DEF=Homo sapiens, similar to ribosomal protein L31, clone MGC:1641, mRNA, complete cds. /FEA=mrna /PROD=Similar to ribosomal protein L31 /DB_XREF=gi:12804504 /UG=Hs.164170 vascular Rab-GAPTC-containing /FL=gb:BC001663.1
214202_at	Consensus includes gb:N21364 /FEA=EST /DB_XREF=gi:1126534 /DB_XREF=est:yx50h10.s1 /CLONE=IMAGE:265219 /UG=Hs.26968 Homo sapiens mRNA from chromosome 5q21-22, clone:357Ex
203142_s_at	gb:NM_003664.1 /DEF=Homo sapiens adaptor-related protein complex 3, beta 1 subunit (AP3B1), mRNA. /FEA=mrna /GEN=AP3B1 /PROD=adaptor-related protein complex 3, beta 1 subunit /DB_XREF=gi:4501974 /UG=Hs.155172 adaptor-related protein complex 3, beta 1 subunit /FL=gb:U91931.1 gb:U81504.1 gb:NM_003664.1
222001_x_at	Consensus includes gb:A1160126 /FEA=EST /DB_XREF=gi:3693506 /DB_XREF=est:qb51h08.x1 /CLONE=IMAGE:1703679 /UG=Hs.295901 KIAA0493 protein
213374_x_at	Consensus includes gb:AW000964 /FEA=EST /DB_XREF=gi:5847880 /DB_XREF=est:wr90h10.x1 /CLONE=IMAGE:2495011 /UG=Hs.236642 3-hydroxyisobutyryl-Coenzyme A hydrolase
201018_at	Consensus includes gb:AL079283.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROTIMAGE 39515. /FEA=mrna /DB_XREF=gi:5102744 /UG=Hs.4310 eukaryotic translation initiation factor 1A /FL=gb:BC000793.1 gb:LI8960.1 gb:NM_001412.1
206206_at	gb:NM_005582.1 /DEF=Homo sapiens lymphocyte antigen 64 (mouse), radioprotective, 105kd (L164), mRNA. /FEA=mrna /GEN=LY64 /PROD=lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kd /DB_XREF=gi:5031894 /UG=Hs.87205 lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kd /FL=gb:D83597.1 gb:NM_005582.1

209566_at	Consensus includes gb:AL080184.1 /DEF=Homo sapiens mRNA; cDNA DKF2p4340071 (from clone DKF2p4340071). /FEA=mRNA / DB_XREF=gi:5262661 /UG=Hs.7089 insulin induced protein 2 /FL=gb:AF125392.1
212194_s_at	Consensus includes gb:AI418892 /FEA=EST /DB_XREF=gi:4264823 /DB_XREF=est:tf43c01.x1 /CLONE=IMAGE:2098944 /UG=Hs.79305 KIAA0255 gene product
204526_s_at	gb:NM_007063.1 /DEF=Homo sapiens vascular Rab-GAPTC-containing (VRP), mRNA. /FEA=mRNA /GEN=VRP /PROD=vascular Rab-GAPTC-containing /DB_XREF=gi:5902153 /UG=Hs.164170 vascular Rab-GAPTC-containing /FL=gb:AB024057.1 gb:NM_007063.1
201568_at	gb:NM_014402.1 /DEF=Homo sapiens low molecular mass ubiquitinone-binding protein (9.5kd) (QP-C), mRNA. /FEA=mRNA /GEN=QP-C /PROD=low molecular mass ubiquitinone-binding protein /DB_XREF=gi:7657485 /UG=Hs.3709 low molecular mass ubiquitinone-binding protein (9.5kd) /FL=gb:BC001390.1 gb:DS0369.1 gb:NM_014402.1
221829_s_at	Consensus includes gb:AI307759 /FEA=EST /DB_XREF=gi:4002363 /DB_XREF=est:tb24g08.x1 /CLONE=IMAGE:2055326 /UG=Hs.168075 karyopherin (importin) beta 2
200613_at	gb:NM_004068.1 /DEF=Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA. /FEA=mRNA /GEN=AP2M1 / PROD=adaptor-related protein complex 2, mu 1 subunit /DB_XREF=gi:4757993 /UG=Hs.152936 adaptor-related protein complex 2, mu 1 subunit /FL=gb:U36188.1 gb:BC004996.1 gb:D63475.1 gb:NM_004068.1
213160_at	Consensus includes gb:D86964.1 /DEF=Human mRNA for KIAA0209 gene, partial cds. /FEA=mRNA /GEN=KIAA0209 /DB_XREF=gi:1504001 / UG=Hs.17211 dedicator of cyto-kinesis 2
211375_s_at	gb:AF141870.1 /DEF=Homo sapiens translational control protein 80 mRNA, complete cds. /FEA=mRNA /PROD=translational control protein 80 /DB_XREF=gi:5006601 /UG=Hs.256583 interleukin enhancer binding factor 3, 90kd /FL=gb:AF141870.1
202276_at	gb:NM_006304.1 /DEF=Homo sapiens Deleted in split-handsplit-foot 1 region (DSS1), mRNA. /FEA=mRNA /GEN=DSS1 /PROD=deleted in split-handsplit-foot 1 region /DB_XREF=gi:5453639 /UG=Hs.85215 Deleted in split-handsplit-foot 1 region /FL=gb:U41515.1 gb:NM_006304.1
201892_s_at	gb:NM_000884.1 /DEF=Homo sapiens IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA. /FEA=mRNA /GEN=IMPDH2 /PROD=IMP (inosine monophosphate) dehydrogenase 2 /DB_XREF=gi:4504688 /UG=Hs.75432 IMP (inosine monophosphate) dehydrogenase 2 / FL=gb:J04208.1 gb:NM_000884.1
217905_at	gb:NM_024834.1 /DEF=Homo sapiens hypothetical protein FLJ13081 (FLJ13081), mRNA. /FEA=mRNA /GEN=FLJ13081 /PROD=hypothetical protein FLJ13081 /DB_XREF=gi:13376242 /UG=Hs.180638 hypothetical protein FLJ13081 /FL=gb:BC004183.1 gb:NM_024834.1
209036_s_at	gb:BC001917.1 /DEF=Homo sapiens; malate dehydrogenase 2, NAD (mitochondrial) /DB_XREF=gi:12804928 /UG=Hs.111076 malate dehydrogenase 2, FEA=mRNA /PROD=malate dehydrogenase 2, NAD (mitochondrial) /DB_XREF=gi:12804928 /UG=Hs.111076 malate dehydrogenase 2, NAD (mitochondrial) /FL=gb:BC001917.1 gb:AF047470.1 gb:NM_005918.1
222010_at	Consensus includes gb:BF224073 /FEA=EST /DB_XREF=gi:11131299 /DB_XREF=est:q83e05.x1 /CLONE=IMAGE:3704936 /UG=Hs.278544 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
203825_at	gb:NM_007371.2 /DEF=Homo sapiens bromodomain-containing 3 (BRD3), mRNA. /FEA=mRNA /GEN=BRD3 /PROD=bromodomain-containing protein 3 /DB_XREF=gi:12408642 /UG=Hs.86896 bromodomain-containing 3 /FL=gb:NM_007371.2 gb:D26362.1
202943_s_at	gb:K38083.1 /DEF=Human alpha-N-acetylgalactosaminidase mRNA, complete cds. /FEA=mRNA /PROD=alpha-N-acetylgalactosaminidase / DB_XREF=gi:189054 /UG=Hs.75372 N-acetylgalactosaminidase, alpha- /FL=gb:BC000095.1 gb:M2783.1 gb:M38083.1 gb:NM_000262.1
210555_s_at	gb:U85430.1 /DEF=Human transcription factor NFATx4 mRNA, complete cds. /FEA=mRNA /PROD=transcription factor NFATx4 / DB_XREF=gi:1835590 /UG=Hs.172674 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 /FL=gb:U85430.1 gb:NM_022753.1
218370_s_at	gb:NM_022753.1 /DEF=Homo sapiens hypothetical protein FLJ12903 (FLJ12903), mRNA. /FEA=mRNA /GEN=FLJ12903 /PROD=hypothetical protein FLJ12903 /DB_XREF=gi:12232418 /UG=Hs.14928 hypothetical protein FLJ12903 /FL=gb:NM_022753.1
208070_s_at	gb:NM_002912.1 /DEF=Homo sapiens REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L), mRNA. /FEA=mRNA / GEN=REV3L /PROD=REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /DB_XREF=gi:4506482 /UG=Hs.115521 REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /FL=gb:AF078695.1 gb:NM_002912.1 gb:AF179428.1
201272_at	gb:NM_001628.1 /DEF=Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA. /FEA=mRNA /GEN= AKR1B1 /PROD=aldo-keto reductase family 1, member B1 (aldose reductase) /DB_XREF=gi:4502048 /UG=Hs.75313 aldo-keto reductase family 1, member B1 (aldose reductase) /FL=gb:BC000260.1 gb:BC005387.1 gb:J04795.1 gb:J0505474.1 gb:M34720.1
209824_s_at	gb:AB000812.1 /DEF=Homo sapiens mRNA for RNAL1b, complete cds. /FEA=mRNA /PROD=RNAL1b /DB_XREF=gi:2094734 /UG=Hs.74515 acyl hydrocarbon receptor nuclear translocator-like /FL=gb:AB000812.1 gb:AF044288.1
209064_x_at	gb:AL136920.1 /DEF=Homo sapiens mRNA; cDNA DKF2p586C051 (from clone DKF2p586C051); complete cds. /FEA=mRNA /GEN=DKF2p586C051 / PROD=hypothetical protein /DB_XREF=gi:12053334 /UG=Hs.109643 polyadenylate binding protein-interacting protein 1 /FL=gb:AL136920.1

200759_x_at	gb:NM_003204.1 /DEF=Homo sapiens nuclear factor (erythroid-derived 2)-like 1 (NFE2L1), mRNA. /FEA=mRNA /GEN=NFE2L1 / PROD=transcription factor 11 (basic leucine zipper type) /DB_XREF=gi:4505378 /UG=Hs.83469 nuclear factor (erythroid-derived 2)-like 1 / FL=gb:NM_003204.1 gb:U08853.1
221787_at	Consensus includes gb:BF431618 /FEA=EST /DB_XREF=gi:11443732 /DB_XREF=est:701603.x1 /CLONE=IMAGE:3574349 /UG=Hs.12342 Homo sapiens clone 24538 mRNA sequence
211581_x_at	gb:AF000426.1 /DEF=Homo sapiens L5T1 mRNA, cluster splice variant, complete cds. /FEA=mRNA /GEN=L5T1 /DB_XREF=gi:2145067 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:AF000426.1
37384_at	Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(106,1470) /gb=D13640 /gi=286006 /ug=Hs.77961 /len=5134
218423_x_at	gb:NM_016516.1 /DEF=Homo sapiens tumor antigen SLP-8p (HCC8), mRNA. /FEA=mRNA /GEN=HCC8 /PROD=tumor antigen SLP-8p /DB_XREF=gi:7705396 /UG=Hs.48499 tumor antigen SLP-8p /FL=gb:AF102177.1 gb:NM_016516.1
210213_s_at	gb:AF022229.1 /DEF=Homo sapiens translation initiation factor 6 (eIF6) mRNA, complete cds. /FEA=mRNA /GEN=eIF6 / PROD=translation initiation factor 6 /DB_XREF=gi:2809382 /UG=Hs.5215 integrin beta 4 binding protein /FL=gb:AF022229.1
201598_s_at	gb:NM_001567.2 /DEF=Homo sapiens inositol polyphosphate phosphatase-like 1 (INPP1), mRNA. /FEA=mRNA /GEN=INPP1 / PROD=inositol polyphosphate phosphatase-like 1 /DB_XREF=gi:4755141 /UG=Hs.75339 inositol polyphosphate phosphatase-like 1 / FL=gb:NM_001567.2 gb:L24444.1
204301_at	gb:NM_014867.1 /DEF=Homo sapiens KIAA0711 gene product (KIAA0711), mRNA. /FEA=mRNA /GEN=KIAA0711 /PROD=KIAA0711 gene product /DB_XREF=gi:7662259 /UG=Hs.5333 KIAA0711 gene product /FL=gb:AB018254.1 gb:NM_014867.1
202877_s_at	Consensus includes gb:W72082 /FEA=EST /DB_XREF=gi:1382588 /DB_XREF=est:zd70c06.s1 /CLONE=IMAGE:345994 /UG=Hs.97199 complement component C1q receptor /FL=gb:NM_012072.2 gb:U94333.1
208772_at	Consensus includes gb:AUI160676 /FEA=EST /DB_XREF=gi:11022197 /DB_XREF=est:AUI160676 /CLONE=Y79AA1002208 /UG=Hs.301226 KIAA1085 protein /FL=gb:AL136943.1
201998_at	Consensus includes gb:AT743792 /FEA=EST /DB_XREF=gi:5112080 /DB_XREF=est:w53h11.x1 /CLONE=IMAGE:2368869 /UG=Hs.2554 sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) /FL=gb:NM_003032.1
208722_s_at	gb:BC001081.1 /DEF=Homo sapiens, anaphase-promoting complex subunit 5, clone MGC:2750, mRNA, complete cds. /FEA=mRNA / PROD=anaphase-promoting complex subunit 5 /DB_XREF=gi:12654502 /UG=Hs.7101 anaphase-promoting complex subunit 5 / FL=gb:BC001081.1 gb:BC001950.1 gb:AF191339.1 gb:NM_016237.1
55692_at	Cluster Incl. W22924:75H3 Homo sapiens cDNA /clone=(not-directional) /gb=W22924 /gi=1299757 /ug=Hs.96560 /len=792
217954_s_at	gb:NM_015153.1 /DEF=Homo sapiens KIAA0244 protein (KIAA0244), mRNA. /FEA=mRNA /GEN=KIAA0244 /PROD=KIAA0244 protein /DB_XREF=gi:7662017 /UG=Hs.78893 KIAA0244 protein /FL=gb:AF091622.1 gb:NM_015153.1
220307_at	gb:NM_016382.1 /DEF=Homo sapiens natural killer cell receptor 2B4 (CD244), mRNA. /FEA=mRNA /GEN=CD244 /PROD=natural killer cell receptor 2B4 /DB_XREF=gi:7706528 /UG=Hs.157872 natural killer cell receptor 2B4 /FL=gb:AF242540.1 gb:AF105261.1 gb:AF145782.1 gb:AF10761.2 gb:AF11771.1 gb:NM_016382.1
211989_at	Consensus includes gb:NM_003079.1 /DEF=Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA. /FEA=CDS /GEN=SMARCE1 /PROD=SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 /DB_XREF=gi:4507088 /UG=Hs.332848 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 /FL=gb:NM_003079.1
209303_at	gb:BC005270.1 /DEF=Homo sapiens, NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase), clone MGC:12313, mRNA, complete cds. /FEA=mRNA /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) /DB_XREF=gi:13528959 /UG=Hs.10758 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) /FL=gb:BC005270.1 gb:AF020351.1 gb:NM_002495.1
201729_s_at	gb:NM_014680.1 /DEF=Homo sapiens KIAA0100 gene product (KIAA0100), mRNA. /FEA=mRNA /GEN=KIAA0100 /PROD=KIAA0100 gene product /DB_XREF=gi:7661903 /UG=Hs.151761 KIAA0100 gene product /FL=gb:D43947.1 gb:NM_014680.1
203530_s_at	gb:NM_004604.1 /DEF=Homo sapiens syntaxin 4A (placental) (STX4A), mRNA. /FEA=mRNA /GEN=STX4A /PROD=syntaxin 4A (placental) /DB_XREF=gi:4759185 /UG=Hs.83734 syntaxin 4A (placental) /FL=gb:BC002436.1 gb:AF026007.1 gb:U07158.1 gb:NM_004604.1
201622_at	gb:NM_014390.1 /DEF=Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA. /FEA=mRNA /GEN=p100 /PROD=EBNA-2 co-activator (100kD) /DB_XREF=gi:7657430 /UG=Hs.75093 EBNA-2 co-activator (100kD) /FL=gb:NM_014390.1 gb:U22055.1

Tabelle 2: Gene aus Clusteranalyse 2

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
200654_at	gb:J02783.1 /DEF=human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mrna /GEN=P4HB /DB_XREF=gi:339646 /UG=Hs.75655procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (DB_XREF=gi:302783.1 gb:NM_000918.1)
203126_at	gb:NM_014214.1 /DEF=Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /FEA=mrna /GEN=IMPA2 /PROD=inositol(myo)-1(or 4)-monophosphatase 2 /DB_XREF=gi:7657235 /UG=Hs.5753 inositol(myo)-1(or 4)-monophosphatase 2. /FL=gb:AF200432.1gb:NM_014214.1 gb:AF014398.2
203585_at	gb:NM_007150.1 /DEF=Homo sapiens zinc finger protein 185 (LIM domain) (ZNF185), mRNA. /FEA=mrna /GEN=ZNF185 /PROD=zinc finger protein 185 (LIM domain) /DB_XREF=gi:6005971 /UG=Hs.16622 zinc finger protein 185 (LIM domain) /FL=gb:NM_007150.1
205220_at	gb:NM_006018.1 /DEF=Homo sapiens putative chemokine receptor; GTP-binding protein (HM74), mRNA. /FEA=mrna /GEN=HM74 /PROD=putative chemokine receptor; GTP-binding protein /DB_XREF=gi:5174460 /UG=Hs.137555 putative chemokine receptor; GTP-binding protein /FL=gb:NM_006018.1
207008_at	gb:NM_001557.1 /DEF=Homo sapiens interleukin 8 receptor, beta (IL8RB), mRNA. /FEA=mrna /GEN=IL8RB /PROD=interleukin 8 receptor, beta /DB_XREF=gi:4504682 /UG=Hs.846 interleukin 8 receptor, beta /FL=gb:M73969.1 gb:NM_001557.1 gb:U19593.1
200897_s_at	gb:NM_016081.1 /DEF=Homo sapiens palladin (KIAA0992), mRNA. /FEA=mrna /GEN=KIAA0992 /PROD=palladin /DB_XREF=gi:7706354 /UG=Hs.194431 palladin /FL=gb:AF077041.1 gb:AF151909.1 gb:NM_016081.1
205568_at	gb:NM_020980.2 /DEF=Homo sapiens aquaporin 9 (AQP9), mRNA. /FEA=mrna /GEN=AQP9 /PROD=aquaporin 9 /DB_XREF=gi:7789059 /DB_XREF=est:ny11d02.sl /CLONE=IMAGE:1271427 /UG=Hs.104624 aquaporin 9 /FL=gb:NM_020980.2 gb:AB008775.1 gb:AF016495.1
214022_s_at	Consensus includes gb:AA749101 /FEA=EST /DB_XREF=gi:7789059 /DB_XREF=est:ny11d02.sl /CLONE=IMAGE:1271427 /UG=Hs.146360 interferon induced transmembrane protein 1 (9-27)
209762_x_at	gb:AF280094.1 /DEF=Homo sapiens transcriptional coactivator Sp110b mRNA, complete cds. /FEA=mrna /PROD=transcriptional coactivator Sp110b /DB_XREF=gi:9800493 /UG=Hs.38125 interferon-induced protein 75, 52kd /FL=gb:AF280094.1
203234_at	gb:NM_003364.1 /DEF=Homo sapiens uridine phosphorylase (UP), mRNA. /FEA=mrna /GEN=UP /PROD=uridine phosphorylase /DB_XREF=gi:4507838 /UG=Hs.77573 uridine phosphorylase /FL=gb:BC001405.1 gb:NM_003364.1
201940_at	Consensus includes gb:AA897514 /FEA=EST /DB_XREF=gi:3034134 /DB_XREF=est:aj62b12.sl /CLONE=IMAGE:1394879 /UG=Hs.5057 carboxypeptidase D /FL=gb:U65090.1 gb:DB5330.1 gb:NM_001304.2
209310_s_at	gb:U25804.1 /DEF=Human Ich-2 cysteine protease mRNA, complete cds. /FEA=mrna /PROD=Ich-2 /DB_XREF=gi:886049 /UG=Hs.74122 caspase 4, apoptosis-related cysteine protease /FL=gb:U28976.1 gb:U28977.1 gb:U28978.1 gb:NM_001225.1 gb:U25804.1 gb:U28014.1
202128_at	gb:NM_014821.1 /DEF=Homo sapiens KIAA0317 gene product (KIAA0317), mRNA. /FEA=mrna /GEN=KIAA0317 /PROD=KIAA0317 gene product /DB_XREF=gi:7662051 /UG=Hs.20126 KIAA0317 gene product /FL=gb:AB002315.1 gb:NM_014821.1
201192_s_at	gb:NM_006224.1 /DEF=Homo sapiens phosphotidylinositol transfer protein (PITPN), mRNA. /FEA=mrna /GEN=PITPN /PROD=phosphotidylinositol transfer protein /DB_XREF=gi:5453907 /UG=Hs.79709 phosphotidylinositol transfer protein /FL=gb:D30036.1 gb:M73704.1 gb:NM_006224.1
208012_x_at	gb:NM_004509.1 /DEF=Homo sapiens interferon-induced protein 41, 30kd (IFI41), mRNA. /FEA=mrna /GEN=IFI41 /PROD=interferon-induced protein 41, 30kd /DB_XREF=gi:4758585 /UG=Hs.241510 interferon-induced protein 41, 30kd /FL=gb:L22342.1 gb:NM_004509.1
209137_s_at	gb:EC000263.1 /DEF=Homo sapiens, Similar to ubiquitin c-terminal hydrolase related polypeptide, clone MGC:2621, mRNA, complete cds. /FEA=mrna /PROD=Similar to ubiquitin c-terminal hydrolase related polypeptide /DB_XREF=gi:12653004 /UG=Hs.78829 ubiquitin specific protease 10 /FL=gb:BC000263.1
218023_s_at	gb:NM_016605.1 /DEF=Homo sapiens putative nuclear protein (LOC51307), mRNA. /FEA=mrna /GEN=LOC51307 /PROD=putative nuclear protein /DB_XREF=gi:7706138 /UG=Hs.102469 putative nuclear protein /FL=gb:AF251040.1 gb:NM_016605.1
201190_s_at	Consensus includes gb:H15647 /FEA=EST /DB_XREF=gi:880467 /DB_XREF=est:ym27b09.sl /CLONE=IMAGE:49287 /UG=Hs.79709 phosphotidylinositol transfer protein /FL=gb:D30036.1 gb:M73704.1 gb:NM_006224.1

210563_x_at	gb:U97075.1 /DEF-Homo sapiens FLICE-like inhibitory protein short form mRNA, complete cds. /FEA-mRNA / PROD=FLICE-like inhibitory protein short form /DB_XREF=gi:2253680 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator / FL=gb:U97075.1 Consensus includes gb:BF788439 /FEA-EST /DB_XREF=gi:10209637 /DB_XREF=est:601475616F1 /CLONE=IMAGE:3878643 /
221827_at	UG=Hs.247280 HBV associated factor gb:NM_004214.3 /DEF-Homo sapiens fibroblast growth factor (acidic) intracellular binding protein (FIBP), mRNA. / FEA-mRNA /GEN=FIBP /PROD=fibroblast growth factor (acidic) intracellular binding protein /DB_XREF=gi:7262377 / UG=Hs.7768 fibroblast growth factor (acidic) intracellular binding protein /FL=gb:AF171944.1 gb:AF171945.1 gb:AF171946.1 gb:AF010187.2 gb:NM_004214.3 Consensus includes gb:EG164064 /FEA-EST /DB_XREF=gi:12670767 /DB_XREF=est:602334109F1 /CLONE=IMAGE:4449022 / UG=Hs.75875 ubiquitin-conjugating enzyme E2 variant 1 /FL=gb:U39361.1 gb:NM_003349.2 gb:BC000468.1 Consensus includes gb:AB020677.2 /DEF-Homo sapiens mRNA for KIAA0870 protein, partial cds. /FEA-mRNA /GEN=KIAA0870 / PROD=KIAA0870 protein /DB_XREF=gi:6635136 /UG=Hs.18166 KIAA0870 protein gb:NM_014045.1 /DEF-Homo sapiens DKFZP564C1940 protein (DKFZP564C1940), mRNA. /FEA-mRNA /GEN=DKFZP564C1940 / PROD=DKFZP564C1940 protein /DB_XREF=gi:13027587 /UG=Hs.3804 DKFZP564C1940 protein. /FL=gb:BC000424.1 gb:NM_014045.1 gb:AF131760.1 Consensus includes gb:NM_002600.1 /DEF-Homo sapiens phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4 (PDE4B) mRNA. /FEA-mRNA /GEN=PDE4B /PROD=phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) / DB_XREF=gi:4505662 /UG=Hs.188 phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) / FL=gb:N97515.1 gb:U20971.1 gb:NM_002600.1
203708_at	gb:NM_014869.1 /DEF-Homo sapiens KIAA0763 gene product /FL=gb:AB018306.1 gb:NM_014869.1 DB_XREF=gi:7662289 /UG=Hs.4764 KIAA0763 gene product /FEA-mRNA /GEN=KIAA0763 /PROD=KIAA0763 gene product /
203907_s_at	gb:AF084462.1 /DEF-Homo sapiens GTP-binding protein ROCI (ROCI) mRNA, complete cds. /FEA-mRNA /GEN=ROCI / PROD=GTP-binding protein ROCI /DB_XREF=gi:4234917 /UG=Hs.96038 Rici (Drosophila)-like, expressed in many tissues / FL=gb:U71203.1 gb:U78165.1 gb:AF084462.1 gb:NM_006912.1
209882_at	Consensus includes gb:BE95437 /FEA-EST /DB_XREF=gi:10358829 /DB_XREF=est:601437912F1 /CLONE=IMAGE:39222971 / UG=Hs.274701 thymidine kinase 2, mitochondrial /FL=gb:NM_004614.1 gb:U77088.1
204276_at	Consensus includes gb:AL040896 /FEA-EST /DB_XREF=gi:5409841 /DB_XREF=est:DKFZp434I2415_s1 /CLONE=DKFZp434I2415 / UG=Hs.22412 hypothetical protein MGC3035
221984_s_at	gb:NM_024900.1 /DEF-Homo sapiens hypothetical protein FLJ22479 (FLJ22479), mRNA. /FEA-mRNA /GEN=FLJ22479 / PROD=hypothetical protein FLJ22479 /DB_XREF=gi:13376356 /UG=Hs.238246 hypothetical protein FLJ22479 /FL=gb:NM_024900.1
218517_at	Consensus includes gb:BF93650 /FEA-EST /DB_XREF=gi:11685974 /DB_XREF=est:nac02d03.x1 /CLONE=IMAGE:3275957 / UG=Hs.23964 sin3-associated polypeptide, 18kD /FL=gb:NM_005870.2 gb:U96915.1 gb:AF153608.1 gb:U78303.1
208740_at	Consensus includes gb:BF691447 /FEA-EST /DB_XREF=gi:11976855 /DB_XREF=est:602247615F1 /CLONE=IMAGE:4332866 / UG=Hs.107526 UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 /FL=gb:AB004550.1 gb:AF038663.1 gb:NM_004776.1
221484_at	gb:BC001903.1 /DEF-Homo sapiens, similar to interleukin 10 receptor, beta, clone MGC:2210, mRNA, complete cds. / FEA-mRNA /PROD=similar to interleukin 10 receptor, beta /DB_XREF=gi:12804902 /UG=Hs.173936 interleukin 10 receptor beta /FL=gb:BC001903.1 gb:NM_000628.1
209575_at	gb:NM_006842.1 /DEF-Homo sapiens splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA. /FEA-mRNA /GEN=SF3B2 / PROD=splicing factor 3b, subunit 2, 145kD /DB_XREF=gi:5803154 /UG=Hs.75916 splicing factor 3b, subunit 2, 145kD / FL=gb:U41371.1 gb:NM_006842.1
200619_at	Consensus includes gb:BC001805.1 /DEF-Homo sapiens, clone IMAGE:3543670, mRNA, partial cds. /FEA-mRNA / PROD=Unknown (protein for IMAGE:3543670) /DB_XREF=gi:12804742 /UG=Hs.240615 hypothetical protein FLJ13556 similar to N-myc downstream regulated 3
217286_s_at	gb:NM_007359.1 /DEF-Homo sapiens MLN51 protein (MLN51), mRNA. /FEA-mRNA /GEN=MLN51 /PROD=MLN51 protein / DB_XREF=gi:6678887 /UG=Hs.83422 MLN51 protein /FL=gb:NM_007359.1
207842_s_at	gb:NM_004481.2 /DEF-Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GALNAC-T2) (GALNT2), mRNA. /FEA-mRNA /GEN=GALNT2 /PROD=polypeptide N-acetylgalactosaminyltransferase 2 / DB_XREF=gi:9945385 /UG=Hs.130181 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GALNAC-T2) /FL=gb:NM_004481.2
217788_s_at	

48612_at	Cluster Incl. AA225490:nc25b01.r1 Homo sapiens cDNA /clone=IMAGE-1009129 /gb=AA225490 /gi=1846817 /ug=Hs.80115 /len=539
212689_s_at	Consensus includes gb:AA524505 /FEA=EST /DB_XREF=gi:2265433 /DB_XREF=est:ing43g12.sl /CLONE=IMAGE:937606 /UG=Hs.321707 KIAA0742 protein
222047_s_at	Consensus includes gb:AA523895 /FEA=EST /DB_XREF=gi:4438030 /DB_XREF=est:tg97g03.x1 /CLONE=IMAGE:2116756 /UG=Hs.111801 arsenate resistance protein ARS2
201666_at	gb:NM_003254.1 /DEF=Homo sapiens tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA. /FEA=mRNA /GEN=TIIMP1 /PROD=tissue inhibitor of metalloproteinase 1 precursor /DB_XREF=gi:4507508 /UG=Hs.5831 tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) /FL=gb:BC000866.1 gb:M12670.1 gb:M59906.1 gb:NM_003254.1
203218_at	Consensus includes gb:W37431 /FEA=EST /DB_XREF=gi:1319025 /DB_XREF=est:zc1fl1.sl /CLONE=IMAGE:322029 /UG=Hs.246857 mitogen-activated protein kinase 9 /FL=gb:U34821.1 gb:NM_002752.1 gb:L31951.1 gb:U09759.1
213118_at	Consensus includes gb:AL136821.1 /DEF=Homo sapiens mRNA; cDNA DKFp434M1526 (from clone DKFp434M1526). /FEA=mRNA /GEN=DKFp434M1526 /PROD=hypothetical protein /DB_XREF=gi:12053152 /UG=Hs.153293 KIAA0701 protein
201057_s_at	gb:NM_004487.1 /DEF=Homo sapiens golgi autoantigen, golgin subfamily b, macrogolin (with transmembrane signal), 1 /mRNA. /FEA=mRNA /GEN=GOLGB1 /PROD=golgi autoantigen, golgin subfamily b, macrogolin (with transmembrane signal), 1 /DB_XREF=gi:4758453 /UG=Hs.7844 golgi autoantigen, golgin subfamily b, macrogolin (with transmembrane signal), 1 /FL=gb:NM_004487.1
217738_at	Consensus includes gb:BF575514 /FEA=EST /DB_XREF=gi:11649318 /DB_XREF=est:602133090F1 /CLONE=IMAGE:4288079 /UG=Hs.239138 pre-B-cell colony-enhancing factor /FL=gb:U02020.1 gb:NM_005746.1
208648_at	Consensus includes gb:W60953 /FEA=EST /DB_XREF=gi:1367731 /DB_XREF=est:zc98b12.sl /CLONE=IMAGE:339167 /UG=Hs.106357 valosin-containing protein /FL=gb:AF100752.1 gb:NM_007126.2
212242_at	Consensus includes gb:AL565074 /FEA=EST /DB_XREF=gi:12916087 /DB_XREF=est:AL565074 /CLONE=CSODN003VF20 (3 prime) /UG=Hs.75318 tubulin, alpha 1 (testis specific)
203897_at	Consensus includes gb:BE963444 /FEA=EST /DB_XREF=gi:11766863 /DB_XREF=est:601657224R1 /CLONE=IMAGE:3866357 /UG=Hs.28607 hypothetical protein A-211C6.1 /FL=gb:NM_020424.1
209513_s_at	gb:BC004331.1 /DEF=Homo sapiens, similar to RIKEN cDNA 2610207116 gene, clone MGC:10940, mRNA, complete cds. /FEA=mRNA /PROD=similar to RIKEN cDNA 2610207116 gene /DB_XREF=gi:13279253 /UG=Hs.47986 Homo sapiens, similar to RIKEN cDNA 2610207116 gene, clone MGC:10940, mRNA, complete cds. /FL=gb:BC004331.1
211762_s_at	gb:BC005978.1 /DEF=Homo sapiens, karyopherin alpha 2 (RAG cohort 1, importin alpha 1), clone MGC:14668, mRNA, complete cds. /FEA=mRNA /PROD=karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /DB_XREF=gi:13543656 /FL=gb:BC005978.1
219639_x_at	gb:NM_020213.1 /DEF=Homo sapiens hypothetical protein from EUROMIMAGE 1977056 (LOC56965), mRNA. /FEA=mRNA /GEN=LOC56965 /PROD=hypothetical protein from EUROMIMAGE 1977056 /DB_XREF=gi:9910373 /UG=Hs.315687 hypothetical protein from EUROMIMAGE 1977056 /FL=gb:NM_020213.1
217882_at	gb:NM_018447.1 /DEF=Homo sapiens 30 kDa protein (LOC55831), mRNA. /FEA=mRNA /GEN=LOC55831 /PROD=30 kDa protein /DB_XREF=gi:8923856 /UG=Hs.283714 30 kDa protein /FL=gb:AF157321.1 gb:NM_018447.1
204714_s_at	gb:NM_000130.2 /DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. /FEA=mRNA /GEN=F5 /PROD=coagulation factor V precursor /DB_XREF=gi:10518500 /UG=Hs.30054 coagulation factor V (proaccelerin, labile factor) /FL=gb:NM_000130.2 gb:M16967.1 gb:M14335.1
221547_at	gb:BC000794.1 /DEF=Homo sapiens, pre-mRNA splicing factor similar to S. cerevisiae Prp18, clone MGC:5075, mRNA, complete cds. /FEA=mRNA /PROD=pre-mRNA splicing factor similar to S. cerevisiae Prp18 /DB_XREF=gi:12653992 /UG=Hs.155244 pre-mRNA processing factor 18 (NUP98) mRNA, complete cds. /FEA=mRNA /GEN=NUP98 /PROD=nucleoporin 98 /FL=gb:U41815.1
210793_s_at	gb:U41815.1 /DEF=Human nucleoporin 98 (NUP98) mRNA, complete cds. /FEA=mRNA /GEN=NUP98 /PROD=nucleoporin 98 /DB_XREF=gi:1184172 /UG=Hs.112255 nucleoporin 98KD /FL=gb:U41815.1
206207_at	gb:NM_001828.3 /DEF=Homo sapiens Charot-Leyden crystal protein (CLC), mRNA. /FEA=mRNA /GEN=CLC /PROD=Charot-Leyden crystal protein /DB_XREF=gi:6325464 /UG=Hs.889 Charot-Leyden crystal protein /FL=gb:L01664.1 gb:NM_001828.3
202595_s_at	gb:AF161461.1 /DEF=Homo sapiens HSPC112 mRNA, complete cds. /FEA=mRNA /PROD=HSPC112 /DB_XREF=gi:6841445.1 /UG=Hs.11000 leptin receptor overexpressed on myeloid cells 1 (TREM1), mRNA. /FEA=mRNA /GEN=TREM1 /PROD=triggering receptor expressed on myeloid cells 1 (TREM1) /DB_XREF=gi:8924261 /UG=Hs.283022 triggering receptor expressed on
219434_at	PROD=triggering receptor expressed on myeloid cells 1 (TREM1) /DB_XREF=gi:8924261 /UG=Hs.283022 triggering receptor expressed on

myeloid cells 1	FL-gb:AF196329.1 gb:NM_018643.1 gb:AF287008.1
205020_s_at	gb:NM_005738.1 /DEF=Homo sapiens ADP-ribosylation factor-like 4 (ARL4), mRNA. /FEA=mRNA /GEN=ARL4 / PROD=ADP-ribosylation factor-like 4 /DB_XREF=gi:5031602 /UG=Hs.201672 ADP-ribosylation factor-like 4 / FL=gb:U73960.1 gb:NM_005738.1
212052_s_at	Consensus includes gb:AB014576.1 /DEF=Homo sapiens mRNA for KIAA0676 protein, partial cds. /FEA=mRNA / GEN=KIAA0676 /PROD=KIAA0676 protein /DB_XREF=gi:3327165 /UG=Hs.155829 KIAA0676 protein gb:NM_003174.2 /DEF=Homo sapiens superinfectin (SVIL), transcript variant 1, mRNA. /FEA=mRNA /GEN=SVIL / PROD=superinfectin, isoform 1 /DB_XREF=gi:11496980 /UG=Hs.154567 superinfectin /FL=gb:NM_003174.2 gb:AF051850.1 gb:AF051851.1
202565_s_at	gb:AF272036.1 /DEF=Homo sapiens Rag D mRNA, complete cds. /FEA=mRNA /PROD=Rag D /DB_XREF=gi:11181619 / UG=Hs.238679 Rag D protein /FL=gb:NM_021244.1 gb:AF272036.1 gb:BC003088.1
221524_s_at	gb:NM_024293.1 /DEF=Homo sapiens hypothetical protein MGC3035 /DB_XREF=gi:13236511 /UG=Hs.22412 hypothetical protein MGC3035 / PROD=hypothetical protein MGC3035 /DB_XREF=gi:13236511 /UG=Hs.22412 hypothetical protein MGC3035 / FL=gb:AL136758.1 gb:BC002420.1 gb:NM_024293.1
218037_at	Consensus includes gb:AW340850 /FEA=EST /DB_XREF=gi:6837476 /DB_XREF=est:xr31f01.x1 /CLONE=IMAGE:2761753 /UG=Hs.326350 Homo sapiens cDNA FLJ11822 f1s, clone HEMBA1006485; highly similar to PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) gb:NM1695.1 /DEF=H. sapiens leukocyte adhesion glycoprotein p150.95 mRNA, complete cds. /FEA=mRNA /GEN=ITGAX / DB_XREF=gi:487829 /UG=Hs.51077 integrin, alpha X (antigen CD11C [p150], alpha polypeptide) /FL=gb:NM1695.1 gb:NM_000887.2
210184_at	gb:U19179.1 /DEF=Human (Hin-2) mRNA, complete cds. /FEA=mRNA /GEN=Hin-2 /DB_XREF=gi:726037 / DB_XREF=gi:487829 /UG=Hs.51077 integrin, alpha X (antigen CD11C [p150], alpha polypeptide) /FL=gb:NM1695.1 gb:NM_000887.2
209107_x_at	gb:U19179.1 /DEF=Human (Hin-2) mRNA, complete cds. /FEA=mRNA /GEN=Hin-2 /DB_XREF=gi:726037 / DB_XREF=gi:487829 /UG=Hs.51077 integrin, alpha X (antigen CD11C [p150], alpha polypeptide) /FL=gb:NM1695.1 gb:NM_000887.2
208749_x_at	gb:AF085357.1 /DEF=Homo sapiens flotillin mRNA, complete cds. /FEA=mRNA /PROD=flotillin /DB_XREF=gi:5114048 / UG=Hs.179986 flotillin 1 /FL=gb:BC001146.1 gb:AF085357.1 gb:AF089750.2 gb:NM_005803.2
212561_at	Consensus includes gb:AA349595 /FEA=EST /DB_XREF=gi:2001934 /DB_XREF=est:EST56429 /UG=Hs.26797 KIAA1091 protein Consensus includes gb:AB011088.1 /DEF=Homo sapiens mRNA for KIAA0516 protein, partial cds. /FEA=mRNA /GEN=KIAA0516 PROD=KIAA0516 protein /DB_XREF=gi:3043555 /UG=Hs.129872 sperm associated antigen 9
212470_at	Consensus includes gb:A1924817 /FEA=EST /DB_XREF=gi:5660781 /DB_XREF=est:wn23c11.x1 /CLONE=IMAGE:2446292 / UG=Hs.75737 pericentriolar material 1
214937_x_at	gb:NM_021975.1 /DEF=Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA. /FEA=mRNA /GEN=RELA / PROD=v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) /DB_XREF=gi:11496238 /UG=Hs.75569 v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) /FL=gb:NM_021975.1 gb:U19067.1
201783_s_at	gb:NM_021188.1 /DEF=Homo sapiens clones 23667 and 23775 zinc finger protein (LOC57862), mRNA. /FEA=mRNA /GEN=LOC57862 / PROD=clones 23667 and 23775 zinc finger protein /DB_XREF=gi:10863994 /UG=Hs.7137 clones 23667 and 23775 zinc finger protein / FL=gb:NM_021188.1 gb:U90919.1
202010_s_at	gb:NM_003641.1 /DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA. /FEA=mRNA /GEN=IFITM1 / PROD=interferon induced transmembrane protein 1 (9-27) /DB_XREF=gi:4504580 /UG=Hs.146360 interferon induced transmembrane protein 1 (9-27) /FL=gb:BC000897.1 gb:U04164.1 gb:NM_003641.1
201601_x_at	gb:NM_003010.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /FEA=mRNA /GEN=MAP2K4 / PROD=mitogen-activated protein kinase kinase 4 /DB_XREF=gi:4506888 /UG=Hs.75217 mitogen-activated protein kinase kinase 4 / FL=gb:NM_003010.1 gb:U17743.1
203266_s_at	gb:NM_016323.1 /DEF=Homo sapiens cyclin-E binding protein 1 (LOC51191), mRNA. /FEA=mRNA /GEN=LOC51191 / PROD=cyclin-E binding protein 1 /DB_XREF=gi:7705930 /UG=Hs.26663 cyclin-E binding protein 1 /FL=gb:AB027289.1 gb:NM_016323.1
219863_at	Consensus includes gb:BE99972 /FEA=EST /DB_XREF=gi:10700248 /DB_XREF=est:7h15b02.x1 /CLONE=IMAGE:3316011 / UG=Hs.186613 sphingosine-1-phosphate lyase 1 /FL=gb:AF144638.1
212322_at	gb:NM_020310.1 /DEF=Homo sapiens MAX binding protein (FL=gb:NM_020310.1 DB_XREF=gi:9945317 /UG=Hs.25497 MAX binding protein /FL=gb:NM_020310.1 DB_XREF=gi:9945317 /UG=Hs.25497 MAX binding protein /FL=gb:NM_020310.1
204206_at	gb:NM_016621.1 /DEF=Homo sapiens hypothetical protein (LOC51317), mRNA. /FEA=mRNA /GEN=LOC51317 / PROD=hypothetical protein /DB_XREF=gi:7706159 /UG=Hs.106826 KIAA1696 protein /FL=gb:AF208848.1 gb:NM_016621.1
203278_s_at	

	gb:NM_014879.1 /DEF=Homo sapiens KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose (KIAA0001), mRNA. /FEA=mRNA /GEN=KIAA0001 /PROD=KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose /DB_XREF=gi:7661847 /UG=Hs.2465 KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose /FL=gb:DI3626.1 gb:NM_014879.1
206637_at	gb:NM_004388.1 /DEF=Homo sapiens chitinase, di-N-acetyl- (CTBS), mRNA. /FEA=mRNA /GEN=CTBS /PROD=chitinase, di-N-acetyl- /DB_XREF=gi:4758091 /UG=Hs.135578 chitinase, di-N-acetyl- /FL=gb:M95767.1 gb:NM_004388.1
218924_s_at	



Tabelle 3: Gene aus Clusteranalyse 3

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
36711_at	Cluster Incl. AL021977:BK447C4.1 (novel MAFP (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein P) E protein) / cds (0.494) / gb=AL021977 / gi=4914526 / ug=Hs.51305 / len=2128
210845_s_at	gb:U08839.1 / DEF=Human urokinase-type plasminogen activator receptor mRNA, complete cds. / FEA-mRNA / PROD=urokinase-type plasminogen activator receptor / DB_XREF=gi:517197 / ug=Hs.179657 / plasminogen activator / FL=gb:U08839.1
202643_s_at	Consensus includes gb:AT738896 / FEA-EST / DB_XREF=gi:5100877 / DB_XREF=est:w122g02.x1 / CLONE=IMAGE:2391026 / ug=Hs.211600 tumor necrosis factor, alpha-induced protein 3 / FL=gb:M59465.1 gb:NM_006290.1
205476_at	gb:NM_004591.1 / DEF=Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA. / FEA-mRNA / GEN=SCYA20 / PROD=small inducible cytokine subfamily A (Cys-Cys), member 20 / DB_XREF=gi:4759075 / ug=Hs.75498 small inducible cytokine subfamily A (Cys-Cys), member 20 / FL=gb:U64197.1 gb:U77035.1 gb:D86955.1 gb:NM_004591.1
205419_at	gb:NM_004951.1 / DEF=Homo sapiens Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) (EBI2), mRNA. / FEA-mRNA / GEN=EBI2 / PROD=Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) / DB_XREF=gi:4826705 / ug=Hs.784 Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) / FL=gb:L08177.1 gb:NM_004951.1
209795_at	gb:L07555.1 / DEF=Homo sapiens early activation antigen CD69 mRNA, complete cds. / FEA-mRNA / PROD=early activation antigen CD69 / DB_XREF=gi:291897 / ug=Hs.82401 CD69 antigen (p60, early T-cell activation antigen) / FL=gb:L07555.1 gb:NM_001781.1
205767_at	gb:NM_001432.1 / DEF=Homo sapiens epiregulin (EREG), mRNA. / FEA-mRNA / GEN=EREG / PROD=epiregulin precursor / DB_XREF=gi:4557566 / ug=Hs.115263 epiregulin / FL=gb:D30783.1 gb:NM_001432.1
203821_at	gb:NM_001945.1 / DEF=Homo sapiens diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA. / FEA-mRNA / GEN=DTR / PROD=diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) / DB_XREF=gi:4503412 / ug=Hs.799 diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) / FL=gb:M60278.1 gb:NM_001945.1
211974_s_at	gb:AY029180.1 / DEF=Homo sapiens soluble urokinase plasminogen activator receptor precursor (SUPAR) mRNA, complete cds. / FEA-mRNA / PROD=supar / PROD=supar / DB_XREF=gi:13641308 / FL=gb:AY029180.1
205403_at	gb:NM_004633.1 / DEF=Homo sapiens interleukin 1 receptor, type II (IL1R2), mRNA. / FEA-mRNA / GEN=IL1R2 / PROD=interleukin 1 receptor, type II / DB_XREF=gi:4758597 / ug=Hs.25333 interleukin 1 receptor, type II / FL=gb:U74649.1 gb:NM_004633.1
204351_at	gb:NM_005980.1 / DEF=Homo sapiens S100 calcium-binding protein P (S100P), mRNA. / FEA-mRNA / GEN=S100P / PROD=S100 calcium-binding protein P / DB_XREF=gi:5174662 / ug=Hs.2962 S100 calcium-binding protein P / FL=gb:NM_005980.1
206115_at	gb:NM_004430.1 / DEF=Homo sapiens early growth response 3 (EGR3), mRNA. / FEA-mRNA / GEN=EGR3 / PROD=early growth response 3 / DB_XREF=gi:4758251 / ug=Hs.74088 early growth response 3 / FL=gb:NM_004430.1
204103_at	gb:NM_002984.1 / DEF=Homo sapiens small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA. / FEA-mRNA / GEN=SCYA4 / PROD=small inducible cytokine A4 (homologous to mouse Mip-1b) / DB_XREF=gi:4506844 / ug=Hs.75703 small inducible cytokine A4 (homologous to mouse Mip-1b) / FL=gb:J04130.1 gb:NM_002984.1 gb:M23502.1 gb:M25316.1
206522_at	gb:NM_004668.1 / DEF=Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. / FEA-mRNA / GEN=MGAM / PROD=alpha-glucosidase / DB_XREF=gi:4758711 / ug=Hs.122785 maltase-glucoamylase (alpha-glucosidase) / FL=gb:AF016833.1 gb:NM_004668.1
202147_s_at	gb:NM_001550.1 / DEF=Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA. / FEA-mRNA / GEN=IFRD1 / PROD=interferon-related developmental regulator 1 / DB_XREF=gi:4504606 / ug=Hs.7879 interferon-related developmental regulator 1 / FL=gb:BC001272.1 gb:NM_001550.1
206515_at	gb:NM_000896.1 / DEF=Homo sapiens cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3), mRNA. / FEA-mRNA / GEN=CYP4F3 / PROD=cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) / DB_XREF=gi:4503240 / ug=Hs.106242 cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) / FL=gb:A8002454.1 gb:D12620.1 gb:NM_000896.1
204614_at	gb:NM_002575.1 / DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINE2), mRNA. / FEA-mRNA / GEN=SERPINE2 / PROD=serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 / DB_XREF=gi:4505594 /

	UG-Hs.75716 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 /FL=gb:J02685.1 gb:J03603.1
	gb:MI8082.1 gb:NM_002575.1
	gb:U12767.1 /DEF=Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds. /FEA=mrna /GEN=MINOR /
	PROD=mitogen induced nuclear orphan receptor /DB_XREF=gi:924281 /UG-Hs.80561 nuclear receptor subfamily 4, group A,
209959_at	member 3 /FL=gb:U12767.1
	Consensus includes gb:AL050388.1 /DEF=Homo sapiens mRNA; cDNA DKFp564M2422 (from clone DKFp564M2422); partial cds. /
	FEA=mrna /GEN=DKFp564M2422 /PROD=hypothetical protein /DB_XREF=gi:4914612 /UG-Hs.306320 Homo sapiens mRNA; cDNA DKFp564M2422
215078_at	(from clone DKFp564M2422); partial cds
	Consensus includes gb:BE966236 /FEA=EST /DB_XREF=gi:1171437 /DB_XREF=est:601660172R1 /CLONE=TWAGE:3905920 /UG-Hs.75319
201890_at	ribonucleotide reductase M2 polypeptide /FL=gb:NM_001034.1
	gb:BC005020.1 /DEF=Homo sapiens, peptidylprolyl isomerase F (cyclophilin F), clone MGC:11022, mRNA, complete cds. /FEA=mrna /
	PROD=peptidylprolyl isomerase F (cyclophilin F) /DB_XREF=gi:13477126 /UG-Hs.173125 peptidylprolyl isomerase F (cyclophilin F) /
201489_at	FL=gb:BC005020.1 gb:M80254.1 gb:NM_005729.1
	gb:NM_000361.1 /DEF=Homo sapiens thrombomodulin (THBD), mRNA. /FEA=mrna /GEN=THBD /PROD=thrombomodulin /DB_XREF=gi:4507482 /
203888_at	UG-Hs.2030 thrombomodulin /FL=gb:NM_15552.1 gb:NM_000361.1
	gb:NM_014059.1 /DEF=Homo sapiens RGC32 protein (RGC32), mRNA. /FEA=mrna /GEN=RGC32 /PROD=RGC32 protein /DB_XREF=gi:7662650 /
218723_s_at	UG-Hs.76640 RGC32 protein /FL=gb:AF036549.1 gb:NM_014059.1
	gb:NM_000519.2 /DEF=Homo sapiens hemoglobin, delta (HBD), mRNA. /FEA=mrna /GEN=HBD /PROD=hemoglobin, delta /DB_XREF=gi:6633803
205834_at	UG-Hs.36977 hemoglobin, delta /FL=gb:NM_000519.2
	gb:NM_002658.1 /DEF=Homo sapiens plasminogen activator, urokinase (PLAU), mRNA. /FEA=mrna /GEN=PLAU /PROD=plasminogen activator,
205479_s_at	urokinase /DB_XREF=gi:4505862 /UG-Hs.77274 plasminogen activator, urokinase /FL=gb:M15476.1 gb:NM_002658.1
	gb:NM_001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mrna /GEN=ADM /PROD=adrenomedullin /DB_XREF=gi:4501944 /
202912_at	gb:NM_001124.1 /FL=gb:NM_001124.1 gb:DL4874.1
	gb:NM_001124.1 /DEF=Homo sapiens GABA-A receptor-associated protein like 1 (GABARAPL1) mRNA, complete cds. /FEA=mrna /
	GEN=GABARAPL1 /PROD=GABA-A receptor-associated protein like 1 /DB_XREF=gi:13375570 /UG-Hs.282654 Homo sapiens mRNA;
208869_s_at	cDNA DKFp564M1272 (from clone DKFp564M1272); complete cds. /FL=gb:AL136676.1 gb:AF087847.1
	gb:NM_005569.2 /DEF=Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA. /FEA=mrna /GEN=LIMK2 /
202193_at	PROD=LIM domain kinase 2 isoform 2a /DB_XREF=gi:8051619 /UG-Hs.278027 LIM domain kinase 2 /FL=gb:D45906.1 gb:NM_005569.2
	Consensus includes gb:AF070569.1 /DEF=Homo sapiens clone 24659 mRNA sequence. /FEA=mrna /DB_XREF=gi:3387938 /UG-Hs.29206
214696_at	Homo sapiens clone 24659 mRNA sequence
	Cluster Incl. M60278:Human heparin-binding EGF-like growth factor mRNA, complete cds /cds=(261.887) /gb=M60278 /gi=183866 /
38037_at	ug-Hs.799 /len=2342
	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA F1J11718 f1s, clone HEMBA1005252, highly similar to Homo sapiens mRNA
212723_at	for KIAA0585 protein. /FEA=mrna /DB_XREF=gi:10433034 /UG-Hs.72660 phosphatidylserine receptor
	gb:NM_006061.1 /DEF=Homo sapiens specific granule protein (28 kDa); cysteine-rich secretory protein-3 (SGP28), mRNA. /FEA=mrna /
	GEN=SGP28 /PROD=specific granule protein (28 kDa); cysteine-rich secretory protein-3 /DB_XREF=gi:5174674 /UG-Hs.54431 specific
207802_at	granule protein (28 kDa); cysteine-rich secretory protein-3 /FL=gb:NM_006061.1
	gb:DL4826.1 /DEF=Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds. /FEA=mrna /
	hCREM=hCREM-2; hCREM-2; hCREM-2 /PROD=hCREM 2beta-b protein; hCREM 2beta-a protein; hCREM 2beta-b protein; hCREM 2beta-a protein;
209967_s_at	hCREM 2alpha-a protein /DB_XREF=gi:532036 /UG-Hs.155924 CAMP responsive element modulator /FL=gb:AF069065.1 gb:DL4826.1
	gb:U73191.1 /DEF=Human inward rectifier potassium channel (KIR1.3), complete cds. /FEA=mrna /GEN=KIR1.3 /PROD=inward rectifier
	potassium channel /DB_XREF=gi:1765984 /UG-Hs.17287 potassium inwardly-rectifying channel, subfamily J, member 15 /
210119_at	FL=gb:U73191.1 gb:NM_002243.1
	gb:NM_007287.1 /DEF=Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, CALLA, CD10) (MEME),
	transcript variant 1b1s, mRNA. /FEA=mrna /GEN=MEME /PROD=membrane metallo-endopeptidase /DB_XREF=gi:6042199 /UG-Hs.1298
203435_s_at	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) /FL=gb:J03779.1 gb:NM_007287.1 gb:NM_007288.1
	Consensus includes gb:AL133353 /FEA=EST /DB_XREF=gi:6360669 /DB_XREF=est:HA1957 /UG-Hs.298161 myosin, light polypeptide 4,
213515_x_at	alkali; atrial, embryonic
	gb:AF064824.1 /DEF=Homo sapiens CARD-containing ICE associated kinase mRNA, complete cds. /FEA=mrna /PROD=CARD-containing ICE.
	associated kinase /DB_XREF=gi:3390171 /UG-Hs.103755 receptor-interacting serine-threonine kinase 2 /FL=gb:BC004553.1
209545_s_at	gb:AF07706.1 gb:AF064824.1 gb:AF078530.1 gb:NM_003821.1
	Consensus includes gb:NM_005564.1 /DEF=Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA. /FEA=cds /GEN=LCN2 /
212531_at	PROD=lipocalin 2 (oncogene 24p3) /DB_XREF=gi:5031852 /UG-Hs.204238 lipocalin 2 (oncogene 24p3) /FL=gb:NM_005564.1

208470_s_at	gb:NM_020995.1 / DEF=Homo sapiens haptoglobin-related protein (HPR), mRNA. / FEA=CD5 / GEN=HPR / PROD=haptoglobin-related protein / DB_XREF=gi:10337588 / UG=Hs.328822 haptoglobin-related protein / FL=gb:NM_020995.1
200733_s_at	gb:U48296.1 / DEF=Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds. / FEA=mrna / GEN=hPTPCAAX1 / PROD=protein tyrosine phosphatase PTPCAAX1 / DB_XREF=gi:1777754 / UG=Hs.227777 protein tyrosine phosphatase type IVA, member 1 / FL=gb:U48296.1 gb:NM_003463.1
211372_s_at	gb:U64094.1 / DEF=human soluble type II interleukin-1 receptor mRNA, complete cds. / FEA=mrna / PROD=soluble type II interleukin-1 receptor / DB_XREF=gi:148065 / UG=Hs.25333 interleukin 1 receptor, type II / FL=gb:U64094.1
204794_at	gb:NM_004418.2 / DEF=Homo sapiens dual specificity phosphatase 2 (DUSP2), mRNA. / FEA=mrna / GEN=DUSP2 / PROD=dual specificity phosphatase 2 / DB_XREF=gi:12707363 / UG=Hs.1183 / dual specificity phosphatase 2 / FL=gb:NM_004418.2 gb:L11329.1
206177_s_at	gb:NM_000045.2 / DEF=Homo sapiens arginase, liver (ARG1), mRNA. / FEA=mrna / GEN=ARG1 / PROD=arginase, type I / DB_XREF=gi:10947138 / UG=Hs.289057 arginase, liver / FL=gb:NM_000045.2 gb:ML4502.1
205239_at	gb:NM_001657.1 / DEF=Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. / FEA=mrna / GEN=AREG / PROD=amphiregulin (schwannoma-derived growth factor) / DB_XREF=gi:4502198 / UG=Hs.270833 amphiregulin (schwannoma-derived growth factor) / FL=gb:M30704.1 gb:NM_001657.1
207094_at	gb:NM_000634.1 / DEF=Homo sapiens interleukin 8 receptor, alpha (IL8RA), mRNA. / FEA=mrna / GEN=IL8RA / PROD=interleukin 8 receptor, alpha / FL=gb:M68932.1 gb:NM_000634.1 gb:L19591.1
200776_s_at	Consensus includes gb:AL518338 / FEA=EST / DB_XREF=gi:12781021 / DB_XREF=est:ALS18328 / CLONE=CS0DA009YK18 (3 prime) / UG=Hs.155291 KIAA0005 gene product / FL=gb:U613630.1 gb:NM_014670.1
215009_s_at	Consensus includes gb:U92014.1 / DEF=Human clone 121711 defective mariner transposon Hmar2 mRNA sequence. / FEA=mrna / DB_XREF=gi:2052456 / UG=Hs.153527 Homo sapiens pTMS mariner-like transposon mRNA, partial sequence
211302_s_at	gb:L20966.1 / DEF=Human phosphodiesterase mRNA, complete cds. / FEA=mrna / PROD=phosphodiesterase / DB_XREF=gi:347121 / UG=Hs.188 phosphodiesterase 4B, cAMP-specific (cunce (Drosophila)-homolog phosphodiesterase E4) / FL=gb:L20966.1
210512_s_at	gb:AF023375.1 / DEF=Homo sapiens vascular endothelial growth factor mRNA, complete cds. / FEA=mrna / PROD=vascular endothelial growth factor / DB_XREF=gi:3719220 / UG=Hs.73793 vascular endothelial growth factor / FL=gb:M32977.1 gb:AF023375.1
212577_at	Consensus includes gb:AB021221.1 gb:AF091352.1
212577_at	Consensus includes gb:AA868754 / FEA=EST / DB_XREF=gi:2964199 / DB_XREF=est:ak52e09.s1 / CLONE=IMAGE:1409608 / UG=Hs.8118 KIAA0650 protein
2114866_at	Consensus includes gb:X74039.1 / DEF=H. sapiens mRNA for urokinase plasminogen activator receptor. / FEA=mrna / PROD=urokinase plasminogen activator receptor / DB_XREF=gi:456192 / UG=Hs.179657 plasminogen activator, urokinase receptor
2119228_at	gb:NM_018555.2 / DEF=Homo sapiens C2H2-like zinc finger protein (ZNF361), mRNA. / FEA=mrna / GEN=ZNF361 / PROD=ZNF361 / DB_XREF=gi:10092612 / UG=Hs.147644 zinc finger protein 361 / FL=gb:AF251515.2 gb:NM_018555.2 gb:AF272148.1
201574_at	gb:NM_004730.1 / DEF=Homo sapiens eukaryotic translation termination factor 1 (EFTF1), mRNA. / FEA=mrna / GEN=EFTF1 / PROD=eukaryotic translation termination factor 1 / DB_XREF=gi:4759033 / UG=Hs.77324 eukaryotic translation termination factor 1 / FL=gb:U901176.1 gb:M75715.1 gb:NM_004730.1
20209498_at	Consensus includes gb:X16354.1 / DEF=human mRNA for transmembrane carcinoembryonic antigen BOPa (formerly TMI-CEA). / FEA=mrna / PROD=TMI-CEA preprotein / DB_XREF=gi:37197 / UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) / FL=gb:U03858.1
20207630_s_at	gb:NM_001881.1 / DEF=Homo sapiens cAMP responsive element modulator (CREM), mRNA. / FEA=mrna / GEN=CREM / PROD=cAMP responsive element modulator / DB_XREF=gi:4503038 / UG=Hs.155924 cAMP responsive element modulator / FL=gb:NM_001881.1 gb:S68271.1
21210873_x_at	gb:U03891.2 / DEF=Homo sapiens phorbolins I mRNA, complete cds. / FEA=mrna / PROD=phorbolins I / DB_XREF=gi:4895107 / UG=Hs.226307 phorbolins (similar to apolipoprotein B mRNA editing protein) / FL=gb:U03891.2
20204419_x_at	gb:NM_000184.1 / DEF=Homo sapiens hemoglobin, gamma G (HBG2), mRNA. / FEA=mrna / GEN=HBG2 / PROD=hemoglobin, gamma G / DB_XREF=gi:6715606 / UG=Hs.283108 hemoglobin, gamma G
20202988_s_at	gb:NM_020972.1 / DEF=Homo sapiens regulator of G-protein signalling 1 (RGS1), mRNA. / FEA=mrna / GEN=RGS1 / PROD=regulator of G-protein signalling 1 / DB_XREF=gi:4506514 / UG=Hs.75256 regulator of G-protein signalling 1 / FL=gb:NM_002922.1
20209273_s_at	Consensus includes gb:EG387555 / FEA=EST / DB_XREF=gi:13281001 / DB_XREF=est:602412371 / CLONE=IMAGE:4521017 / UG=Hs.177776 Hypothetical protein WGC4276 similar to C8B198 / FL=gb:AF284752.1 gb:BC002675.1
20202693_s_at	Consensus includes gb:AW194730 / FEA=EST / DB_XREF=gi:6473630 / DB_XREF=est:mx43d1.x1 / CLONE=IMAGE:2696469 / UG=Hs.9075 serine/threonine kinase 17a (laptoctosis-inducing) / FL=gb:AB011420.1 gb:NM_004760.1
205270_s_at	gb:NM_005565.2 / DEF=Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) (LCP2), mRNA. / FEA=mrna / GEN=LCP2 / PROD=lymphocyte cytosolic protein 2 / DB_XREF=gi:7382491 / UG=Hs.2488 lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) / FL=gb:NM_005565.2 gb:U20158.1

202284_s.at	gb:NM_000389.1 / DEF=Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), mRNA. / FEA=mRNA / GEN=CDKN1A / PROD=cyclin-dependent kinase inhibitor 1A (p21, Cip1) / FL=gq:NM_000389.1 gb:BC000275.1 gb:BC001935.1 gb:U03106.1 gb:L26165.1 gb:L26165.1 gb:U03106.1 gb:U03106.1 gb:U03106.1
21219471_at	gb:NM_025113.1 / DEF=Homo sapiens hypothetical protein FLJ21562 (FLJ21562), mRNA. / FEA=mRNA / GEN=hypothetical protein FLJ21562 / DB_XREF=gi:13376686 / UG=Hs.288708 hypothetical protein FLJ21562 / FL-gb:NM_025113.1
208651_x.at	gb:M58664.1 / DEF=Homo sapiens CD24 signal transducer mRNA, complete cds. / FEA=mRNA / PROD=signal transducer CD24 / DB_XREF=gi:180167 / UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) / FL-gb:M58664.1 gb:L33930.1
211434_s.at	gb:NM_013230.1 / DEF=Homo sapiens putative chemokine receptor (GRAM-A) mRNA, complete cds. / FEA=mRNA / GEN=GRAM-A / PROD=putative chemokine receptor / DB_XREF=gi:3550066 / UG=Hs.302043 chemokine (C-C motif) receptor-like 2 / FL-gb:AF015524.1
2204285_s.at	Consensus includes gb:A1857639 / FEA=EST / DB_XREF=gi:5511255 / UG=XREF=est:wK95g09.xl / CLONE=IMAGE:2423200 / UG=Hs.96 phorbol-12-myristate-13-acetate-induced protein 1 / FL-gb:NM_021127.1
221824_s.at	Consensus includes gb:AA70170 / FEA=EST / DB_XREF=gi:2821408 / DB_XREF=est:ah84d09.sl / CLONE=1322321 / UG=Hs.288156 Homo sapiens cDNA: FLJ21819 fis, clone HEP011485
219081_at	gb:NM_024668.1 / DEF=Homo sapiens hypothetical protein FLJ20288 (FLJ20288), mRNA. / FEA=mRNA / GEN=FLJ20288 / PROD=hypothetical protein FLJ11979 / DB_XREF=gi:13386461 / UG=Hs.84045 hypothetical protein FLJ20288 / FL-gb:BC004457.1 gb:NM_024668.1
220528_at	gb:NM_018399.1 / DEF=Homo sapiens VNN3 protein (HS2238982), mRNA. / FEA=mRNA / GEN=HS2238982 / PROD=VNN3 protein / DB_XREF=gi:9055235 / UG=Hs.183556 VNN3 protein / FL-gb:NM_018399.1
205896_at	gb:NM_003059.1 / DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. / FEA=mRNA / GEN=SLC22A4 / PROD=solute carrier family 22 (organic cation transporter), member 4 / DB_XREF=gi:4507002 / UG=Hs.77239 solute carrier family 22 (organic cation transporter), member 4 / FL-gb:AB007448.1 gb:NM_003059.1
211445_x.at	gb:AF315951.1 / DEF=Homo sapiens FKSG17 (FKSG17) mRNA, complete cds. / FEA=mRNA / GEN=FKSG17 / DB_XREF=gi:12276119 / UG=Hs.307057 Homo sapiens FKSG17 (FKSG17) mRNA, complete cds / FL-gb:AF315951.1
204286_s.at	gb:NM_021127.1 / DEF=Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. / FEA=mRNA / GEN=PMAIP1 / PROD=phorbol-12-myristate-13-acetate-induced protein1 / DB_XREF=gi:10863322 / UG=Hs.96 phorbol-12-myristate-13-acetate-induced protein 1 / FL-gb:NM_021127.1
202503_s.at	gb:NM_014736.1 / DEF=Homo sapiens KIAA0101 gene product (KIAA0101), mRNA. / FEA=mRNA / GEN=KIAA0101 / PROD=KIAA0101 gene product / DB_XREF=gi:7661905 / UG=Hs.81892 KIAA0101 gene product / FL-gb:DL4657.1 gb:NM_014736.1
211560_s.at	gb:AF130113.1 / DEF=Homo sapiens clone FLB8929 PRO2399 mRNA, complete cds. / FEA=mRNA / PROD=PRO2399 / DB_XREF=gi:11493529 / UG=Hs.79103 cytochrome b5 outer mitochondrial membrane precursor / FL-gb:AF130113.1
209945_s.at	gb:BC000251.1 / DEF=Homo sapiens, similar to glycogen synthase kinase 3 beta, clone MGC:1736, mRNA, complete cds. / FEA=mRNA / PROD=similar to glycogen synthase kinase 3 beta / DB_XREF=gi:12652980 / UG=Hs.78802 glycogen synthase kinase 3 beta / FL-gb:BC000251.1
217997_at	Consensus includes gb:A1795908 / FEA=EST / DB_XREF=gi:5361371 / DB_XREF=est:wh40a05.xl / CLONE=IMAGE:2383184 / UG=Hs.82101 pleckstrin homology-like domain, family A, member 1 / FL-gb:NM_007350.1
203757_s.at	gb:BC005008.1 / DEF=Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. / FEA=mRNA / PROD=carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) / DB_XREF=gi:13477106 / UG=Hs.73848 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) / FL-gb:BC005008.1 gb:M18216.1 gb:M29541.1 gb:NM_002483.1
205269_at	Consensus includes gb:A123351 / FEA=EST / DB_XREF=gi:3539017 / UG=XREF=est:gq47g03.xl / CLONE=IMAGE:1689940 / UG=Hs.2488 lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) / FL-gb:NM_015056.2 gb:U20158.1
219049_at	gb:NM_018371.1 / DEF=Homo sapiens hypothetical protein FLJ11264 (FLJ11264), mRNA. / FEA=mRNA / GEN=FLJ11264 / PROD=hypothetical protein FLJ11264 / DB_XREF=gi:8922959 / UG=Hs.11260 hypothetical protein FLJ11264 / FL-gb:NM_018371.1
209396_s.at	gb:M80927.1 / DEF=Human glycoprotein mRNA, complete cds. / FEA=mRNA / PROD=glycoprotein / DB_XREF=gi:348911 / UG=Hs.75184 chitinase 3-like 1 (cartilage glycoprotein-39) / FL-gb:M80927.1 gb:NM_001276.1
202637_s.at	Consensus includes gb:AI608725 / FEA=EST / DB_XREF=gi:4617892 / UG=XREF=est:tw30b01.xl / CLONE=IMAGE:2266921 / UG=Hs.168383 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor / FL-gb:M24283.1 gb:J03132.1 gb:NM_000201.1
205557_at	gb:NM_001725.1 / DEF=Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA. / FEA=mRNA / GEN=BPI / PROD=bactericidal/permeability-increasing protein (BPI) / DB_XREF=gi:4502446 / UG=Hs.89535 bactericidal/permeability-increasing protein / FL-gb:AF322588.1 gb:J04739.1 gb:NM_001725.1
207072_at	gb:NM_003853.1 / DEF=Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA. / FEA=mRNA / GEN=IL18RAP / PROD=interleukin 18 receptor accessory protein / DB_XREF=gi:4504656 / UG=Hs.158315 interleukin 18 receptor accessory protein / FL-gb:AF077346.1 gb:NM_003853.1

202498_s_at	Consensus includes gb:BES50486 /FEA=EST /DB_XREF=gi:9792178 /DB_XREF=est:a27c01.x1 /CLONE=IMAGE:3219936 /UG=Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3 /FL=gb:M20681.1 gb:NM_006931.1 gb:NM_016006.1 /DEF=Homo sapiens CGI-58 protein (LOC51099). mRNA. /FEA=mrna /GEN=LOC51099 /PROD=CGI-58 protein /DB_XREF=gi:7705770 /UG=Hs.19385 CGI-58 protein /FL=gb:AF151816.1 gb:NM_016006.1
218739_at	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA FJ111718 f1s, clone HEMBA1005252, highly similar to Homo sapiens mRNA for KIAA0585 protein. /FEA=mrna /DB_XREF=gi:10433034 /UG=Hs.72660 phosphatidylserine receptor
212722_s_at	Consensus includes gb:AW576457 /FEA=EST /DB_XREF=gi:7247996 /DB_XREF=est:ui-HF-BR0p-aji-a-01-0-UI.s1 /CLONE=IMAGE:3074568 /UG=Hs.20952 Homo sapiens clone 24411 mRNA sequence
212930_at	gb:NM_000611.1 /DEF=Homo sapiens CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, and G344) (CD59). mRNA. /FEA=mrna /GEN=CD59 /PROD=CD59 antigen p18-20 by monoclonal antibodies 16.3A5, EJ16, EJ30, and G344) /DB_XREF=gi:10833164 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, and G344) /FL=gb:NM_000611.1 gb:M34671.1
200985_s_at	gb:NM_007115.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6). mRNA. /FEA=mrna /GEN=TNFAIP6 /PROD=tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM_007115.1
206026_s_at	gb:AF279372.1 /DEF=Homo sapiens inositol 1,3,4-trisphosphate 56-kinase mRNA, complete cds. /FEA=mrna /PROD=inositol 1,3,4-trisphosphate 56-kinase /DB_XREF=gi:12006345 /UG=Hs.6453 inositol 1,3,4-trisphosphate 56 kinase /FL=gb:AF279372.1
210740_s_at	Consensus includes gb:AA877765 /FEA=EST /DB_XREF=gi:2986730 /DB_XREF=est:nr06f05.s1 /CLONE=IMAGE:1161057 /UG=Hs.811
202333_s_at	ubiquitin-conjugating enzyme E2B (RAD6 homolog) /FL=gb:M74525.1 gb:NM_003337.1
201566_x_at	gb:DI13891.1 /DEF=Human mRNA for Id-2H, complete cds. /FEA=mrna /GEN=Id-2H /PROD=Id-2H /DB_XREF=gi:464183 /UG=Hs.180919
44790_s_at	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /FL=gb:M97796.1 gb:NM_002166.1 gb:DI13891.1
213836_s_at	Cluster Incl. A1129310:qc48a05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1712816 /clone_end=3 /gb=AI129310 /gi=3597824 /UG=Hs.234923 /len=811
205027_s_at	Consensus includes gb:AW052084 /FEA=EST /DB_XREF=gi:5914443 /DB_XREF=est:wy86f07.x1 /CLONE=IMAGE:2555461 /UG=Hs.279937 KIAA1001 protein
207329_at	gb:NM_005204.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase 8 (MAP3K8). mRNA. /FEA=mrna /GEN=MAP3K8 /PROD=mitogen-activated protein kinase kinase kinase 8 /FL=gb:DI14497.1 gb:NM_005204.1
217996_at	gb:NM_002424.1 /DEF=Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8). mRNA. /FEA=mrna /GEN=MMP8 /PROD=matrix metalloproteinase 8 preproprotein /DB_XREF=gi:4505220
208632_at	Consensus includes gb:AA576961 /FEA=EST /DB_XREF=gi:2354435 /DB_XREF=est:nm82d08.s1 /CLONE=IMAGE:1074735 /UG=Hs.82101
206851_at	pleckstrin homology-like domain, family A, member 1 /FL=gb:NM_007350.1
203434_s_at	Consensus includes gb:AL578551 /FEA=EST /DB_XREF=gi:12942733 /DB_XREF=est:AL578551 /CLONE=CS00K001Y001 (3 prime) /UG=Hs.5094 ring finger protein 10 /FL=gb:AB027196.1
216236_s_at	gb:NM_002935.1 /DEF=Homo sapiens ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3). mRNA. /FEA=mrna /GEN=RNASE3 /PROD=ribonuclease, RNase A family, 3 (eosinophil cationic protein) /FL=gb:NM_002935.1 gb:M28128.1
206342_x_at	UG=Hs.73839 ribonuclease, RNase A family, 3 (eosinophil cationic protein) /FL=gb:NM_002935.1
201329_s_at	Consensus includes gb:AI433463 /FEA=EST /DB_XREF=gi:4289355 /DB_XREF=est:ti65g11.x1 /CLONE=IMAGE:2136932 /UG=Hs.1298 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) /FL=gb:J03779.1 gb:NM_007287.1 gb:NM_007288.1
200731_s_at	Consensus includes gb:AL110298.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564K1672 (from clone DKFZp564K1672); partial cds. /FEA=mrna /GEN=DKFZp564K1672 /PROD=hypothetical protein /DB_XREF=gi:5817258 /UG=Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3
212508_at	gb:NM_006123.1 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS). transcript variant 2, mRNA. /FEA=mrna /GEN=IDS /PROD=iduronate-2-sulfatase isoform b precursor /DB_XREF=gi:5360207 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:L40586.1 gb:NM_006123.1
201329_s_at	PROD=v-ets avian erythroblastosis virus E26 oncogene homolog 2 /DB_XREF=gi:4885220 /UG=Hs.85146 v-ets avian erythroblastosis virus E26 oncogene homolog 2 (ETS2). mRNA. /FEA=mrna /GEN=ETS2
200731_s_at	Consensus includes gb:AK024029.1 /DEF=Homo sapiens cDNA FJ113967 f1s, clone Y79AA1001402, weakly similar to Homo sapiens tyrosine phosphatase type IVA, member 1 /FL=gb:U48296.1 gb:NM_003463.1
212508_at	Consensus includes gb:AK024029.1 /DEF=Homo sapiens cDNA FJ113967 f1s, clone Y79AA1001402, weakly similar to Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA. /FEA=mrna /DB_XREF=gi:10436287 /UG=Hs.24719 modulator of apoptosis 1 /

[illegible]



37028_at	Cluster Incl. U83981.Homo.sapiens apoptosis associated protein (GADD34) mRNA, complete cds /cds=(222,2246) /gb=U83981 /gi=3258617 /ug=Hs.76556 /len=2331
40446_at	Cluster Incl. AL021366:c10K0721Q.4.1 (PHD finger protein 2) (isoform 2) /cds=(215,1918) /gb=AL021366 /gi=3169115 /ug=Hs.166204 /len=2260
219062_s_at	gb:NM_017742.1 /DEF=Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA. /FEA-mRNA /GEN=FLJ20281 /PROD=hypothetical protein FLJ20281 /DB_XREF=gi:18923259 /UG=Hs.18800 hypothetical protein FLJ20281 /FL=gb:NM_017742.1
202158_s_at	gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA-mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1
60084_at	Cluster Incl. A1453099:tj61ell.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2146028 /clone_end=3 /gb=A1453099 /gi=4307988 /ug=Hs.24668 /len=554
210142_x_at	gb:AF117234.1 /DEF=Homo sapiens flotillin mRNA, complete cds. /FEA-mRNA /PROD=flotillin /DB_XREF=gi:6563241 /UG=Hs.179986 flotillin 1 /FL=gb:AF117234.1
204490_s_at	gb:M24915.1 /DEF=Human CD44 antigen, complete cds. /FEA-mRNA /DB_XREF=gi:180196 /UG=Hs.169610 CD44 antigen (homolog function and Indian blood group system) /FL=gb:NM_000610.1 gb:U40373.1 gb:M59040.1 gb:M24915.1
203949_at	gb:NM_000250.1 /DEF=Homo sapiens myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA. /FEA-mRNA /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:4557758 /UG=Hs.1817 myeloperoxidase /FL=gb:M19507.1 gb:M02694.1 gb:NM_000250.1
219259_at	gb:NM_022367.1 /DEF=Homo sapiens hypothetical protein FLJ2287 similar to semaphorins (FLJ2287), mRNA. /FEA-mRNA /GEN=FLJ2287 /PROD=hypothetical protein FLJ2287 similar to semaphorins /DB_XREF=gi:11641290 /UG=Hs.7634 hypothetical protein FLJ2287 similar to semaphorins /FL=gb:NM_022367.1 gb:AB029394.1
201751_at	gb:NM_014876.1 /DEF=Homo sapiens KIAA0063 gene product (KIAA0063), mRNA. /FEA-mRNA /GEN=KIAA0063 /PROD=KIAA0063 gene product /DB_XREF=gi:7661887 /UG=Hs.3094 KIAA0063 gene product /FL=gb:D31884.1 gb:NM_014876.1
203153_at	gb:NM_001548.1 /DEF=Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), mRNA. /FEA-mRNA /GEN=IFIT1 /PROD=interferon-induced protein with tetratricopeptide repeats 1 /DB_XREF=gi:4504584 /UG=Hs.20315 interferon-induced protein with tetratricopeptide repeats 1 /FL=gb:M24594.1 gb:NM_001548.1
210724_at	gb:AF239764.1 /DEF=Homo sapiens EGF-like module-containing mucin-like receptor EMR3 mRNA, complete cds. /FEA-mRNA /PROD=EGF-like module-containing mucin-like receptor EMR3 mRNA, complete cds /FL=gb:AF239764.1 /UG=Hs.32677 Homo sapiens EGF-like module-containing mucin-like receptor EMR3 mRNA, complete cds
202381_at	gb:NM_003816.1 /DEF=Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA. /FEA-mRNA /GEN=ADAM9 /PROD=a disintegrin and metalloproteinase domain 9 (meltrin gamma) /FL=gb:U41766.1 gb:NM_003816.1
217824_at	Consensus includes gb:X16447.1 /DEF=Human mRNA for CD59, an LY-6-like protein regulating complement membrane attack. /CLONE=IMAGE:3077105 /UG=Hs.184325 CGI-76 protein /FL=gb:AF151834.1 gb:AF161502.1 gb:AF151039.1 gb:NM_016021.1
200984_s_at	Consensus includes gb:AW500009 /FEA=EST /DB_XREF=gi:7112213 /DB_XREF=est:U1-HP-BN0-aki-e-09-0-U1.r1 /FEA-mRNA /PROD=precursor polypeptide (AA -25 to 103) /DB_XREF=gi:29805 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EJ32 and G344) /FL=gb:NM_000611.1 gb:M34671.1
219999_at	gb:NM_018621.1 /DEF=Homo sapiens hypothetical protein PRO2198 (PRO2198), mRNA. /FEA-mRNA /GEN=PRO2198 /PROD=hypothetical protein PRO2198
212644_s_at	Consensus includes gb:AL671747 /FEA=EST /DB_XREF=gi:4851478 /DB_XREF=est:wa05e06.x1 /CLONE=IMAGE:2297218 /UG=Hs.81360 Homo sapiens cDNA: FLJ21927 f18, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence
219622_at	gb:NM_017817.1 /DEF=Homo sapiens hypothetical protein FLJ20429 (FLJ20429), mRNA. /FEA-mRNA /GEN=FLJ20429 /PROD=hypothetical protein FLJ20429 /DB_XREF=gi:8923400 /UG=Hs.179791 hypothetical protein FLJ20429 /FL=gb:NM_017817.1
219190_s_at	gb:NM_017629.1 /DEF=Homo sapiens hypothetical protein FLJ20033 (FLJ20033), mRNA. /FEA-mRNA /GEN=FLJ20033 /PROD=hypothetical protein FLJ20033 /DB_XREF=gi:8923033 /UG=Hs.134757 hypothetical protein FLJ20033 /FL=gb:NM_017629.1
208707_at	Consensus includes gb:BE552334 /FEA=EST /DB_XREF=gi:9794026 /DB_XREF=est:hy06c06.x1 /CLONE=IMAGE:3196522 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1
218506_x_at	gb:NM_018459.1 /DEF=Homo sapiens uncharacterized bone marrow protein BM045 /DB_XREF=gi:8922103 /GEN=BM045 /PROD=uncharacterized bone marrow protein BM045 /FL=gb:AF217521.1 gb:NM_018459.1
207545_s_at	gb:NM_003744.1 /DEF=Homo sapiens numb (Drosophila) homolog (NUMB), mRNA. /FEA-mRNA /GEN=NUMB /PROD=numb (Drosophila) homolog /DB_XREF=gi:4505478 /UG=Hs.78890 numb (Drosophila) homolog /FL=gb:NM_003744.1 gb:L40393.1

212014_x_at	Consensus includes gb:AT493245 /FEA=EST /DB_XREF=gi:4394248 /DB_XREF=est:ti30d08.x1 /CLONE=IMAGE:2131983 /UG=Hs.169610 CD44 antigen (homolog function and Indian blood group system)
209039_x_at	gb:AF001434.1 /DEF=Human Hoast (HPAST) mRNA, complete cds. /FEA=mrna /GEN=HPAST /PROD=HPAST /DB_XREF=gi:2529706 /UG=Hs.155119 EH domain containing 1 /FL=gb:AF001434.1
208650_s_at	Consensus includes gb:BG327863 /FEA=EST /DB_XREF=gi:13134301 /DB_XREF=est:602426876F1 /CLONE=IMAGE:4564675 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:M58664.1 gb:L31930.1 gb:NM_013230.1
209806_at	gb:BC000893.1 /DEF=Homo sapiens, H2B histone family, member A, clone MGC:5132, mRNA, complete cds. /FEA=mrna /PROD=H2B histone family, member A /DB_XREF=gi:12654150 /UG=Hs.247817 H2B histone family, member A /FL=gb:BC000893.1
212573_at	Consensus includes gb:AF131747.1 /DEF=Homo sapiens clone 24951 mRNA sequence. /FEA=mrna /DB_XREF=gi:4406562 /UG=Hs.167115 KIAA0830 protein
203845_at	Consensus includes gb:AV727449 /FEA=EST /DB_XREF=gi:10836870 /DB_XREF=est:AV727449 /CLONE=HWCAYG01 /UG=Hs.199061 p300CBP-associated factor /FL=gb:U57317.2 gb:NM_003884.2
215806_x_at	Consensus includes gb:M13231.1 /DEF=Human T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HPB-MT. /FEA=mrna /DB_XREF=gi:339168 /UG=Hs.274509 T cell receptor gamma constant 2
202195_s_at	gb:NM_016040.1 /DEF=Homo sapiens CGI-100 protein (LOC50999), mRNA. /FEA=mrna /GEN=LOC50999 /PROD=CGI-100 protein
201912_s_at	gb:NM_002094.1 /DEF=Homo sapiens GI to S phase transition 1 (GSPT1), mRNA. /FEA=mrna /GEN=GSPT1 /PROD=GI to S phase transition 1 /DB_XREF=gi:4504166 /UG=Hs.2707 GI to S phase transition 1 /FL=gb:NM_002094.1
201712_s_at	gb:NM_006267.2 /DEF=Homo sapiens RAN binding protein 2 (RANBP2), mRNA. /FEA=mrna /GEN=RANBP2 /PROD=RAN binding protein 2 /DB_XREF=gi:6382078 /UG=Hs.199179 RAN binding protein 2 /FL=gb:NM_006267.2 gb:D42063.1
212864_at	Consensus includes gb:Y16521.1 /DEF=Homo sapiens RAN binding protein 2 (RANBP2), mRNA. /FEA=mrna /GEN=RANBP2 /PROD=CDS2 protein /DB_XREF=gi:4186022 /UG=Hs.24812 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
203504_s_at	gb:NM_005502.1 /DEF=Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABC1), mRNA. /FEA=mrna /GEN=ABC1 /PROD=ATP-binding cassette, sub-family A (ABC1), member 1 /DB_XREF=gi:5915657 /UG=Hs.211562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 gb:NM_005502.1 gb:AF285167.1
212457_at	Consensus includes gb:AL161985.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761J1810 (from clone DKFZp761J1810). /FEA=mrna /DB_XREF=gi:7328121 /UG=Hs.274184 transcription factor binding to IGHM enhancer 3
214683_s_at	Consensus includes gb:AI251890 /FEA=EST /DB_XREF=gi:3848419 /DB_XREF=est:qu78d12.x1 /CLONE=IMAGE:1978199 /UG=Hs.2083 CDC-like kinase1
44783_s_at	Cluster Incl. R61374:vh15e02.sl Homo sapiens cDNA, 3' end /clone=IMAGE-37665 /clone_end=3 /gb=R61374 /gi=832069 /ug=Hs.234434 /len=434
202522_at	gb:NM_002870.1 /DEF=Homo sapiens RAB13, member RAS oncogene family /DB_XREF=gi:4506362 /UG=Hs.151536 RAB13, member RAS oncogene family /FL=gb:BC000799.1
206025_s_at	Consensus includes gb:AM188198 /FEA=EST /DB_XREF=gi:642634 /DB_XREF=est:x193f03.x1 /CLONE=IMAGE:2664797 /UG=Hs.29352 tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM_007115.1
203936_s_at	gb:NM_004994.1 /DEF=Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD type IV collagenase) (MMP9), mRNA. /FEA=mrna /GEN=MMP9 /PROD=matrix metalloproteinase 9 preproprotein /DB_XREF=gi:4826835 /UG=Hs.151738 matrix metalloproteinase 9 (gelatinase B, 92kD type IV collagenase) /FL=gb:J05070.1 gb:NM_004994.1
221523_s_at	Consensus includes gb:AL138717 /DEF=Human DNA sequence from clone RP11-11D8 on chromosome 6 Contains the 5' end of the gene for a yeast ubiquitin conjugating enzyme UBC6 homolog, the gene for a possible grp binding protein, a NACA (nascent polypeptide-associated complex alpha polypeptide... /FEA=mrna, 2 /DB_XREF=gi:8894207 /UG=Hs.238679 Rag D protein /FL=gb:NM_021244.1 gb:AF272036.1 gb:BC003088.1
215785_s_at	Consensus includes gb:AL161999.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mrna /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein
217822_at	gb:NM_016312.1 /DEF=Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA. /FEA=mrna /GEN=LOC51729 /PROD=Npw38-binding protein NpwBP /DB_XREF=gi:7706500 /UG=Hs.16420 Npw38-binding protein NpwBP /FL=gb:BC001621.1 gb:AF118023.1 gb:AB029309.1 gb:NM_016312.1
202206_at	Consensus includes gb:AW450363 /FEA=EST /DB_XREF=gi:6991139 /DB_XREF=est:UT-H-B13-aka-d-02-0-UI.sl /CLONE=IMAGE:2734875 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
202439_s_at	gb:NM_000202.2 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA. /FEA=mrna /GEN=IDS /PROD=iduronate-2-sulfatase isoform a precursor /DB_XREF=gi:5360215 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:M58342.1 gb:NM_000202.2



213056_at	Consensus includes gb:AUI45019 /FEA-EST /DB_XREF=gi:11006540 /DB_XREF=est:AUI45019 /CLONE=HEMBA1003646 /UG=Hs.96427 KIAA1013 protein
222142_at	Consensus includes gb:AK024212.1 /DEF=Homo sapiens cDNA FLJ14150 fis, clone WAMWA1003026, highly similar to Homo sapiens HSPC057 mRNA. /FEA-mRNA /DB_XREF=gi:10436534 /UG=Hs.18827 KIAA0849 protein
214784_x_at	Consensus includes gb:BE966299 /FEA-EST /DB_XREF=gi:11711566 /DB_XREF=est:601660539R1 /CLONE=IMAGE:3906248 /UG=Hs.70500 KIAA0370 protein
222035_s_at	Consensus includes gb:A1984479 /FEA-EST /DB_XREF=gi:5811756 /DB_XREF=est:wr83e06.x1 /CLONE=IMAGE:2494306 /UG=Hs.49007 poly(A) polymerase alpha
212219_at	Consensus includes gb:D38521.1 /DEF=human mRNA for KIAA0077 gene, partial cds. /FEA-mRNA /GEN=KIAA0077 /DB_XREF=gi:559329 /UG=Hs.112396 KIAA0077 protein
214152_at	Consensus includes gb:AUI44243 /FEA-EST /DB_XREF=gi:11005764 /DB_XREF=est:AUI44243 /CLONE=HEMBA1001328 /UG=Hs.247118 phosphatidylinositol glycan, class B
202948_at	gb:NM_000877.1 /DEF=Homo sapiens interleukin 1 receptor, type 1 (IL1R1), mRNA. /FEA-mRNA /GEN=IL1R1 /PROD=interleukin 1 receptor, type 1 /DB_XREF=gi:4504658 /UG=Hs.82112 interleukin 1 receptor, type 1 (IL1R1), mRNA. /FEA-mRNA /GEN=NR4A3 /PROD=nuclear receptor subfamily 4, group A, member 3 (NR4A3), mRNA. /FEA-mRNA /GEN=NR4A3 /PROD=nuclear receptor subfamily 4, group A, member 3 /DB_XREF=gi:11276070 /UG=Hs.80561 nuclear receptor subfamily 4, group A, member 3 /FL=gb:NM_006981.1 gb:D78579.1
207978_s_at	gb:AF087853.1 /DEF=Homo sapiens growth arrest and DNA damage inducible protein beta (GADD45B) mRNA, complete cds. /FEA-mRNA /GEN=GADD45B /PROD=growth arrest and DNA damage inducible protein beta /DB_XREF=gi:12061050 /UG=Hs.110571 growth arrest and DNA-damage-inducible, beta /FL=gb:AF087853.1 gb:AF078077.1
209304_x_at	Consensus includes gb:BG177920 /FEA-EST /DB_XREF=gi:12684623 /DB_XREF=est:602327839F1 /CLONE=IMAGE:4429256 /UG=Hs.75510 annexin A11
214783_s_at	Cluster Incl. AL039447:DKFZp434N1010_s1 Homo sapiens cDNA, 3' end /clone=DKFZp434N1010 /clone_end=3 /gb=AL039447 /gi=5408497 /ug=Hs.75425 /len=841
221760_at	Consensus includes gb:BG287153 /FEA-EST /DB_XREF=gi:13040709 /DB_XREF=est:602381868F1 /CLONE=IMAGE:4499393 /UG=Hs.25253 mannosidase, alpha, class 1A, member 1
210118_s_at	gb:NM_000043.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA. /FEA-mRNA /GEN=TNFRSF6 /PROD=apoptosis (APO-1) antigen 1 /DB_XREF=gi:4507582 /UG=Hs.82359 tumor necrosis factor receptor superfamily, member 6 /FL=gb:M67454.1 gb:NM_000043.1
204781_s_at	gb:NM_013416.1 /DEF=Homo sapiens neutrophil cytosolic factor 4 (NCF4), transcript variant 2, mRNA. /FEA-mRNA /GEN=NCF4 /PROD=neutrophil cytosolic factor 4 (NCF4), isoform 2 /DB_XREF=gi:7382492 /UG=Hs.196352 neutrophil cytosolic factor 4 (NCF4) /FL=gb:BC002798.1 gb:AB025219.1 gb:NM_013416.1
207677_s_at	gb:NM_019094.1 /DEF=Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA. /FEA-mRNA /GEN=NUDT4 /PROD=nudix (nucleoside diphosphate linked moiety X)-type motif 4 /DB_XREF=gi:10800135 /UG=Hs.92381 /NUDT4 (nucleoside diphosphate linked moiety X)-type motif 4 /FL=gb:NM_019094.1 gb:AF191649.1 gb:AF191650.1 gb:AF191653.1
206302_s_at	gb:NM_017849.1 /DEF=Homo sapiens hypothetical protein FLJ20507 (FLJ20507), mRNA. /FEA-mRNA /GEN=FLJ20507 /PROD=hypothetical protein FLJ20507 /DB_XREF=gi:8923465 /UG=Hs.202955 hypothetical protein FLJ20507 /FL=gb:NM_017849.1
219460_s_at	Consensus includes gb:AL516854 /FEA-EST /DB_XREF=gi:12780347 /DB_XREF=est:AL516854 /CLONE=CS0DA007YE20 (5 prime) /UG=Hs.150580 putative translation initiation factor
212225_at	gb:NM_012383.1 /DEF=Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /FEA-mRNA /GEN=OSTF1 /PROD=osteoclast stimulating factor 1 /DB_XREF=gi:6912563 /UG=Hs.95821 osteoclast stimulating factor 1 /FL=gb:U63717.1 gb:NM_012383.1
204479_at	Consensus includes gb:AK026080.1 /DEF=Homo sapiens cDNA: FLJ22427 fis, clone HRC09013. /FEA-mRNA /DB_XREF=gi:10438814 /UG=Hs.288883 splicing factor 3a, subunit 1, 120KD
216457_s_at	Consensus includes gb:AW293356 /FEA-EST /DB_XREF=gi:6699992 /DB_XREF=est:U1-H-B12-ahl-c-11-0-UT.s1 /CLONE=IMAGE:2727165 /UG=Hs.58220 Homo sapiens cDNA: FLJ23005 fis, clone UNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence
212676_at	gb:NM_005013.1 /DEF=Homo sapiens nucleobindin 2 (NUCB2), mRNA. /FEA-mRNA /GEN=NUCB2 /PROD=nucleobindin 2 /DB_XREF=gi:4828869 /UG=Hs.3164 nucleobindin 2 /FL=gb:AF052642.1 gb:AF052643.1 gb:AF052644.1 gb:NM_005013.1
203675_at	gb:NM_004748.1 /DEF=Homo sapiens cell cycle progression 8 protein (CPR8), mRNA. /FEA-mRNA /GEN=CPR8 /PROD=cell cycle progression 8 protein /DB_XREF=gi:4758047 /UG=Hs.283753 cell cycle progression 8 protein /FL=gb:AF011794.1 gb:NM_004748.1
221156_x_at	gb:NM_004161.1 /DEF=Homo sapiens RAB1, member RAS oncogene family (RAB1), mRNA. /FEA-mRNA /GEN=RAB1 /PROD=RAB1,
207791_s_at	

	member RAS oncogene family /DB_XREF=gi:4758907 /UG=Hs.3642 RAS1, member RAS oncogene family /FL=gb:NM_004161.1 gb:M28209.1
	gb:NM_004134.1 /DEF=Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B), mRNA. /FEA=mrna /GEN=HSPA9B /PROD=heat shock 70kD protein 9B (mortalin-2) /DB_XREF=gi:4758569 /UG=Hs.3069 heat shock 70kD protein 9B (mortalin-2) /FL=gb:BC000478.1 gb:L15189.1 gb:NM_004134.1
200692_s_at	gb:NM_014167.1 /DEF=Homo sapiens HSPC128 protein (HSPC128), mRNA. /FEA=mrna /GEN=HSPC128 /PROD=HSPC128 protein /DB_XREF=gi:7661789 /UG=Hs.90527 HSPC128 protein /FL=gb:AF213377.1 gb:AF161477.1 gb:NM_014167.1
218936_s_at	Consensus includes gb:A1819238 /FEA=EST /DB_XREF=gi:5438328 /DB_XREF=est:wj42g05.xl /CLONE=IMAGE:2405528 /UG=Hs.180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
219391_at	gb:NM_016626.1 /DEF=Homo sapiens hypothetical protein (LOC51320), mRNA. /FEA=mrna /GEN=LOC51320 /PROD=hypothetical protein /DB_XREF=gi:7706165 /UG=Hs.12830 hypothetical protein /FL=gb:AF208855.1 gb:NM_016626.1
218247_s_at	Consensus includes gb:AF007132.1 /DEF=Homo sapiens clone 23551 mRNA sequence. /FEA=mrna /DB_XREF=gi:2852606 /UG=Hs.184019 Homo sapiens clone 23551 mRNA sequence
213935_at	gb:AB023420.1 /DEF=Homo sapiens mRNA for heat shock protein apg-2, complete cds. /FEA=mrna /GEN=apg-2 /PROD=apg-2 /DB_XREF=gi:4579908 /UG=Hs.90093 heat shock 70kD protein 4 /FL=gb:AB023420.1
208815_x_at	Consensus includes gb:AA293502 /FEA=EST /DB_XREF=gi:1941036 /DB_XREF=est:zt53h06.xl /CLONE=IMAGE:726107 /UG=Hs.42733
218177_at	CHMP1.5 protein /FL=gb:AF281064.1 gb:NM_020412.1
	gb:NM_002065.1 /DEF=Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL), mRNA. /FEA=mrna /GEN=GLUL /PROD=glutamate-ammonia ligase (glutamine synthase) /DB_XREF=gi:4504026 /UG=Hs.170171
200648_s_at	glutamate-ammonia ligase (glutamine synthase) /FL=gb:NM_002065.1
	gb:NM_012328.1 /DEF=Homo sapiens microvascular endothelial differentiation gene 1 (MDG1), mRNA. /FEA=mrna /GEN=MDG1 /PROD=microvascular endothelial differentiation gene 1 /DB_XREF=gi:9558754 /UG=Hs.6790 DnaJ (Hsp40) homolog, subfamily B, member 9 /FL=gb:AF083247.1 gb:AL080081.1 gb:AB026908.1 gb:NM_012328.1
202843_at	Consensus includes gb:AV683882 /FEA=EST /DB_XREF=gi:10285745 /DB_XREF=est:AV683882 /CLONE=GKCAIC05 /UG=Hs.17820
214578_s_at	Rho-associated, coiled-coil containing protein kinase 1 /FL=gb:U43195.1 gb:NM_005406.1
	Consensus includes gb:AF229163 /DEF=Homo sapiens natural resistance-associated macrophage protein 1 (SLC11A1) gene, complete cds, alternatively spliced; and nuclear LIM interactor-interacting factor (NLI-IF) gene, complete cds /FEA=mrna_3 /DB_XREF=gi:10257408 /UG=Hs.182611 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
217473_x_at	gb:NM_000328.1 /DEF=Homo sapiens retinitis pigmentosa GTPase regulator (RPGR), mRNA. /FEA=mrna /GEN=RPGR /PROD=retinitis pigmentosa GTPase regulator /DB_XREF=gi:4506580 /UG=Hs.153614 retinitis pigmentosa GTPase regulator /FL=gb:U57629.1 gb:NM_000328.1
207624_s_at	gb:NM_003453.1 /DEF=Homo sapiens zinc finger protein 198 (ZNF198), mRNA. /FEA=mrna /GEN=ZNF198 /PROD=zinc finger protein 198 /DB_XREF=gi:4508010 /UG=Hs.109526 zinc finger protein 198 /FL=gb:AF035374.1 gb:AF060181.1 gb:NM_003453.1
202778_s_at	gb:M27319.1 /DEF=Human calmodulin mRNA, complete cds. /FEA=mrna /PROD=calmodulin /DB_XREF=gi:179809 /UG=Hs.177656
200653_s_at	calmodulin 1 (phosphorylase kinase, delta) /FL=gb:M27319.1 gb:NM_006888.1
	gb:NM_018370.1 /DEF=Homo sapiens hypothetical protein FLJ11259 (FLJ11259), mRNA. /FEA=mrna /GEN=FLJ11259 /PROD=hypothetical protein FLJ11259 /DB_XREF=gi:8922957 /UG=Hs.184455 hypothetical protein FLJ11259 /FL=gb:NM_018370.1
218627_at	gb:NM_002264.1 /DEF=Homo sapiens karyopherin alpha 1 (importin alpha 5) (KPNA1), mRNA. /FEA=mrna /GEN=KPNA1 /PROD=karyopherin alpha 1 /DB_XREF=gi:4504894 /UG=Hs.169149 karyopherin alpha 1 (importin alpha 5) /FL=gb:BC002374.1
	gb:BC003009.1 gb:NM_002264.1
202059_s_at	gb:NM_024075.1 /DEF=Homo sapiens LENG5 protein (LENG5), mRNA. /FEA=mrna /GEN=LENG5 /PROD=LENG5 protein /DB_XREF=gi:13129061 /UG=Hs.15580 LENG5 protein /FL=gb:BC000944.2 gb:NM_024075.1
218132_s_at	Consensus includes gb:AA810268 /FEA=EST /DB_XREF=gi:2879627 /DB_XREF=est:od14f07.s1 /CLONE=IMAGE:1367941 /UG=Hs.75217 mitogen-activated protein kinase kinase 4 /FL=gb:NM_003010.1 gb:L36870.1 gb:U17743.1
203265_s_at	gb:M97655.1 /DEF=Human 6-pyruvoyltetrahydropterin synthase (PTS) mRNA, complete cds. /FEA=mrna /GEN=PTS /PROD=6-pyruvoyltetrahydropterin synthase /DB_XREF=gi:306438 /UG=Hs.366 6-pyruvoyltetrahydropterin synthase /FL=gb:M97655.1 gb:NM_000317.1 gb:U17400.1
209694_at	Consensus includes gb:BF725121 /FEA=EST /DB_XREF=gi:12041032 /DB_XREF=est:bx12e01.xl /CLONE=bx12e01 /UG=Hs.272108 ESTs
217591_at	
222309_at	Consensus includes gb:AW972292 /FEA=EST /DB_XREF=gi:8162138 /DB_XREF=est:EST384381 /UG=Hs.292998 ESTs

201627_s_at	gb:NM_005542.1 / DEF=Homo sapiens insulin induced gene 1 (INSIG1), mRNA. / FEA=mrna / GEN=INSIG1 / PROD=insulin induced gene 1 / DB_XREF=gi:5031800 / UG=Hs.56205 Insulin induced gene 1 / FL=gb:NM_005542.1
217249_x_at	Consensus includes gb:AC004544 / DEF=Homo sapiens BAC clone CTB-162B4 from 4 / FEA=CDS / DB_XREF=gi:3041843 / UG=Hs.248095 Homo sapiens BAC clone CTB-162B4 from 4
220496_at	gb:NM_016509.1 / DEF=Homo sapiens C-type lectin-like receptor-2 (LOC51266), mRNA. / FEA=mrna / GEN=LOC51266 / PROD=C-type lectin-like receptor-2 / DB_XREF=gi:7706060 / UG=Hs.114231 C-type lectin-like receptor-2 / FL=gb:AF124841.1
201096_s_at	Consensus includes gb:AL537042 / FEA=EST / DB_XREF=gi:12800535 / DB_XREF=est:AL537042 / CLONE=CS0DF017YF17 (5 prime). / UG=Hs.75290 ADP-ribosylation factor 4 / FL=gb:BC003364.1 gb:NM_001660.2
201580_s_at	Consensus includes gb:AL544094 / FEA=EST / DB_XREF=gi:12876573 / DB_XREF=est:AL544094 / CLONE=CS0DI004VG20 (3 prime) / UG=Hs.169358 hypothetical protein / FL=gb:NM_021156.1
201109_s_at	Consensus includes gb:AV726673 / FEA=EST / DB_XREF=gi:10836094 / DB_XREF=est:AV726673 / CLONE=HTC8C12 / UG=Hs.87409 thrombospondin 1 / FL=gb:NM_003246.1
203080_s_at	gb:NM_013450.1 / DEF=Homo sapiens bromodomain adjacent to zinc finger domain, 2B / DB_XREF=gi:7304922 / UG=Hs.8383 bromodomain adjacent to zinc finger domain, 2B / FL=gb:AB032255.1 gb:NM_013450.1
202558_s_at	gb:NM_006948.1 / DEF=Homo sapiens stress 70 protein chaperone, microsome-associated, 60kD / FL=gb:U04735.1 gb:NM_006948.1 / GEN=STCH / PROD=stress 70 protein chaperone, microsome-associated, 60kD / FL=gb:U04735.1 gb:NM_006948.1
201349_at	gb:NM_004252.1 / DEF=Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 / DB_XREF=gi:4759139 / UG=Hs.184276 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 / FL=gb:BC001443.1 gb:NM_004252.1
220603_s_at	gb:NM_018349.1 / DEF=Homo sapiens hypothetical protein FLJ11175 (FLJ11175), mRNA. / FEA=mrna / GEN=FLJ11175 / PROD=hypothetical protein FLJ11175 / DB_XREF=gi:8922916 / UG=Hs.33368 hypothetical protein FLJ11175 / FL=gb:NM_018349.1
35820_at	Cluster incl. X62078:H. sapiens mRNA for GM2 activator protein (cds=UNKNOWN) / gb:X62078 / gi:313158 / UG=Hs.69743 / len=2436 gb:NM_003292.1 / DEF=Homo sapiens translocated promoter region (to activated MTO oncogene) (TPR), mRNA. / FEA=mrna / GEN=TPR / PROD=translocated promoter region (to activated MTO oncogene) / DB_XREF=gi:4507658 / UG=Hs.169750 translocated promoter region (to activated MTO oncogene) / FL=gb:NM_003292.1
201731_s_at	gb:NM_000123.1 / DEF=Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group 5 (Cockayne syndrome)) (ERCC5), mRNA. / FEA=mrna / GEN=ERCC5 / PROD=xpg-complementing protein / DB_XREF=gi:4503600 / UG=Hs.48576 excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group 5 (Cockayne syndrome)) / FL=gb:U0402.1 gb:NM_000123.1
202414_at	gb:NM_000578.1 gb:L20046.1 gb:NM_000123.1
210422_x_at	gb:NM_000578.1 gb:L32185.1
58900_at	Cluster incl. AW025284:wu95h10.x1 Homo sapiens cDNA, 3' end / clone=IMAGE-990806 / clone_end=3 / gb:AW025284 / gi=5878814 / UG=Hs.237946 / len=454
208112_x_at	gb:NM_013252.1 / DEF=Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA. / FEA=mrna / GEN=CLECSF5 / PROD=C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 / DB_XREF=gi:10281668 / UG=Hs.126355 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 / FL=gb:NM_013252.1 gb:AF139768.1
218655_s_at	gb:NM_006795.1 / DEF=Homo sapiens EH domain containing 1 (EHD1), mRNA. / FEA=mrna / GEN=EHD1 / PROD=EH domain containing 1 / DB_XREF=gi:5803008 / UG=Hs.155119 EH domain containing 1 / FL=gb:AF099011.1 gb:NM_006795.1
214230_at	gb:NM_017748.1 / DEF=Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA. / FEA=mrna / GEN=FLJ20291 / PROD=hypothetical protein FLJ20291 / DB_XREF=gi:8923270 / UG=Hs.8928 hypothetical protein FLJ20291 / FL=gb:NM_017748.1
201898_s_at	Consensus includes gb:R37664 / FEA=EST / DB_XREF=gi:795120 / DB_XREF=est:yf61e05.sl / CLONE=IMAGE:26577 / UG=Hs.146409 cell division cycle 42 (GTP-binding protein, 25kD)
	Consensus includes gb:A1126625 / FEA=EST / DB_XREF=gi:3595139 / DB_XREF=est:qd83a12.x1 / CLONE=IMAGE:1736062 / UG=Hs.80612 ubiquitin-conjugating enzyme E2A (RAD6 homolog) / FL=gb:NM_003336.1

210773_s_at	gb:U81501.1 /DEF=Human lipoxin A4 receptor mRNA, complete cds. /FEA=mrna /PROD=lipoxin A4 receptor /DB_XREF=gi:1916075 /UG=Hs.99855 formyl peptide receptor-like 1 /FL=gb:M76672.1 gb:M88107.1 gb:U81501.1 gb:AF054013.1
32069_at	gb:NM_001462.1 Cluster Incl. AB014515: Homo sapiens mRNA for KIAA0615 protein, complete cds /cds=(237,2927) /gb=AB014515 /gi=3327043 /ug=Hs.155972 /len=3319
121_at	X59699 /FEATURE= /DEFINITION=HSPX8A H.sapiens Pax8 mRNA
202053_s_at	gb:L47162.1 /DEF=Human fatty aldehyde dehydrogenase (FALDH) mRNA, complete cds. /FEA=mrna /GEN=FALDH /PROD=fatty aldehyde dehydrogenase /DB_XREF=gi:1082035 /UG=Hs.159608 aldehyde dehydrogenase 3 family, member A2 /FL=gb:L47162.1 gb:U46689.1 gb:NM_000382.1
212335_at	Consensus includes gb:NM167793 /FEA=EST /DB_XREF=gi:6399401 /DB_XREF=est:xg56d07.x1 /CLONE=IMAGE:2632333 /UG=Hs.164036 Homo sapiens AKAP150C mRNA sequence, alternatively spliced
209813_x_at	gb:M16768.1 /DEF=Human T-cell receptor gamma chain VUCl-CII-CIII region mRNA, complete cds. /FEA=mrna /GEN=TCRG /DB_XREF=gi:339399 /UG=Hs.112259 T cell receptor gamma locus /FL=gb:M16768.1 gb:AF151103.1
204747_at	gb:NM_001549.1 /DEF=Homo sapiens interferon-induced protein with tetratricopeptide repeats 4 (IFIT4), mRNA. /FEA=mrna /GEN=IFIT4 /PROD=interferon-induced protein with tetratricopeptide repeats 4 /DB_XREF=gi:4504586 /UG=Hs.181874
212223_at	interferon-induced protein with tetratricopeptide repeats 4 /FL=gb:BC001383.1 gb:BC004977.1 gb:U52513.1 gb:AF026939.1
218880_at	Consensus includes gb:AF083470.1 gb:NM_001549.1
202460_s_at	Consensus includes gb:AI926544 /FEA=EST /DB_XREF=gi:5662508 /DB_XREF=est:wo46c12.x1 /CLONE=IMAGE:2458390 /UG=Hs.303154
58780_s_at	popeye protein 3
205281_s_at	Consensus includes gb:N36408 /FEA=EST /DB_XREF=gi:1157550 /DB_XREF=est:yy33f03.s1 /CLONE=IMAGE:273053 /UG=Hs.325364
218251_at	hypothetical protein FLJ23306 /FL=gb:NM_024530.1
212481_s_at	gb:NM_014646.1 /DEF=Homo sapiens lipin 2 (LPIN2), mRNA. /FEA=mrna /GEN=LPIN2 /PROD=lipin 2 /DB_XREF=gi:7662021.1
213292_s_at	UG=Hs.166318 lipin 2 /FL=gb:D87436.1 gb:NM_014646.1
221497_x_at	Cluster Incl. R42449:yg02a07.s1 Homo sapiens cDNA, 3' end /clones=IMAGE-30831 /clone_end=3 /gb=R42449 /gi=817213 /ug=Hs.235831 /len=431
212185_x_at	gb:NM_002641.1 /DEF=Homo sapiens phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) (PIGA), transcript variant 1, mRNA. /FEA=mrna /GEN=PIGA /PROD=phosphatidylinositol glycan, class A isoform 1 /DB_XREF=gi:11863129
203961_at	UG=Hs.51 phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) /FL=gb:NM_002641.1 gb:DL1466.1
210986_s_at	gb:NM_021242.1 /DEF=Homo sapiens hypothetical protein STRAIT11499 (STRAIT11499), mRNA. /FEA=mrna /GEN=STRAIT11499 /PROD=hypothetical protein STRAIT11499 /DB_XREF=gi:10864050 /UG=Hs.236556 hypothetical protein STRAIT11499 /FL=gb:NM_021242.1
41386_i_at	Consensus includes gb:AT214061 /FEA=EST /DB_XREF=gi:3777662 /DB_XREF=est:ap29d10.x1 /CLONE=IMAGE:1956787 /UG=Hs.250641 tropomyosin 4
201874_at	Consensus includes gb:AA908770 /FEA=EST /DB_XREF=gi:3048175 /DB_XREF=est:ol06a11.s1 /CLONE=IMAGE:1522652 /UG=Hs.283881 KIAA0713 protein
211781_x_at	gb:BC005369.1 /DEF=Homo sapiens, chromosome 1 open reading frame 12, clone MGC:12484, mRNA, complete cds. /FEA=mrna /PROD=chromosome 1 open reading frame 12 /DB_XREF=gi:13529208 /UG=Hs.6523 chromosome 1 open reading frame 12 /FL=gb:NM_022051.1 gb:NM_022051.1 gb:BC005369.1
202459_s_at	FL=gb:AF229245.1 gb:AF227176.1 gb:NM_022051.1 gb:BC005369.1
	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS /GEN=MT2A /PROD=metalothionein 2A /DB_XREF=gi:5174763 /UG=Hs.118786 metallothionein 2A /FL=gb:NM_005953.1
	Consensus includes gb:AL157398 /DEF=Human DNA sequence from clone RP11-56H7 on chromosome 10. Contains ESTs, STSs and GSSs. Contains the gene for the nebulin protein (NEB), actin-binding 2-disc protein) /FEA=mrna_1 /DB_XREF=gi:10045326 /UG=Hs.5025 nebulin /FL=gb:NM_006393.1
	gb:Z24727.1 /DEF=H.sapiens tropomyosin isoform mRNA, complete cds. /FEA=mrna /PROD=tropomyosin isoform /DB_XREF=gi:854188 /UG=Hs.77899 tropomyosin 1 (alpha) /FL=gb:Z24727.1
	Cluster Incl. AB002344: Human mRNA for KIAA0346 gene, partial cds /cds=(0,4852) /gb=AB002344 /gi=2280479 /ug=Hs.103915 /len=6121
	Consensus includes gb:BF978611 /FEA=EST /DB_XREF=gi:12345826 /DB_XREF=est:602149061f1 /CLONE=IMAGE:4307822 /UG=Hs.14891 hypothetical protein FLJ21047 /FL=gb:NM_024569.1
	gb:BC006164.1 /DEF=Homo sapiens, clone MGC:13219, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:13219) /DB_XREF=gi:13544062 /FL=gb:BC006164.1
	Consensus includes gb:U55968 /FEA=EST /DB_XREF=gi:1354524 /DB_XREF=est:HSU55968 /CLONE=26508 /UG=Hs.166318 lipin 2 /FL=gb:D87436.1 gb:NM_014646.1

217908_s_at	gb:NM_018442.1 / DEF=Homo sapiens PC326 protein (PC326), mRNA. / FEA=mrna / GEN=PC326 / PROD=PC326 protein / DB_XREF=gi:8923955 / UG=Hs.279882 PC326 protein / FL=gb:AL136738.1 gb:AF150734.1 gb:NM_018442.1
202427_s_at	gb:NM_015415.1 / DEF=Homo sapiens DKFZP564B167 protein (DKFZP564B167), mRNA. / FEA=mrna / GEN=DKFZP564B167 / PROD=DKFZP564B167 protein / DB_XREF=gi:7661601 / UG=Hs.76285 DKFZP564B167 protein / FL=gb:AL110297.1 gb:NM_015415.1
213716_s_at	Consensus includes gb:BF039675 / FEA=EST / DB_XREF=gi:12357086 / DB_XREF=est:nac7907.xl / CLONE=IMAGE:3440820 / UG=Hs.336612
212550_at	Consensus includes gb:AF149535 / FEA=EST / DB_XREF=gi:3678004 / DB_XREF=est:qc70f11.xl / CLONE=IMAGE:1714989 / UG=Hs.24064 Homo sapiens mRNA; cDNA DKFZP586N1323 (from clone DKFZP586N1323)
33323_r_at	Cluster Incl. X57348:H. sapiens mRNA (clone 9112) / cds=(165,911) / gb=X57348 / UG=Hs.184510 / len=1407
220947_s_at	gb:NM_015527.1 / DEF=Homo sapiens DKFZP434P1750 protein (DKFZP434P1750), mRNA. / FEA=mrna / GEN=DKFZP434P1750 / PROD=DKFZP434P1750 protein / DB_XREF=gi:7661587 / UG=Hs.7274 DKFZP434P1750 protein / FL=gb:NM_015527.1
202665_s_at	gb:NM_003387.2 / DEF=Homo sapiens Wiskott-Aldrich syndrome protein interacting protein (WASP-IP), mRNA. / FEA=mrna / GEN=WASP-IP / PROD=WASP-interacting protein / DB_XREF=gi:8400739 / UG=Hs.24143 Wiskott-Aldrich syndrome protein interacting protein / FL=gb:NM_003387.2
220746_s_at	gb:NM_016290.1 / DEF=Homo sapiens retinoid x receptor interacting protein (LOC51720), mRNA. / FEA=mrna / GEN=LOC51720 / PROD=retinoid x receptor interacting protein / DB_XREF=gi:7706482 / UG=Hs.7889 retinoid x receptor interacting protein / FL=gb:AF113538.1 gb:NM_016290.1
218078_s_at	gb:NM_016598.1 / DEF=Homo sapiens DHHC1 protein (LOC51304), mRNA. / FEA=mrna / GEN=LOC51304 / PROD=DHHC1 protein / DB_XREF=gi:7706132 / UG=Hs.14896 DHHC1 protein / FL=gb:AF247703.1 gb:NM_016598.1
203429_s_at	gb:NM_016227.1 / DEF=Homo sapiens membrane protein CH1 (CH1), mRNA. / FEA=mrna / GEN=CH1 / PROD=membrane protein CH1 / DB_XREF=gi:7705321 / UG=Hs.108636 membrane protein CH1 / FL=gb:AF097535.1 gb:NM_016227.1
203120_at	gb:NM_005426.1 / DEF=Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA. / FEA=mrna / GEN=TP53BP2 / PROD=tumor protein p53-binding protein, 2 / DB_XREF=gi:4885642 / UG=Hs.44595 tumor protein p53-binding protein, 2 / FL=gb:U58334.1 gb:NM_005426.1
203143_s_at	Consensus includes gb:T79953 / FEA=EST / DB_XREF=gi:698462 / DB_XREF=est:yd85c11.s1 / CLONE=IMAGE:115028 / UG=Hs.158282 KIAA0040 gene product / FL=gb:D25539.1 gb:NM_014656.1
41387_r_at	Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds / cds=(0,4852) / gb=AB002344 / UG=Hs.103915 / len=6121
202286_s_at	Consensus includes gb:J04152 / DEF=Human gastrointestinal tumor-associated antigen GA733-1 protein gene, complete cds, clone 05516 / FEA=mrna / DB_XREF=gi:182893 / UG=Hs.23582 tumor-associated calcium signal transducer 2 / FL=gb:NM_002353.1
200670_at	gb:NM_005080.1 / DEF=Homo sapiens X-box binding protein 1 (XBPI), mRNA. / FEA=mrna / GEN=XBPI / PROD=X-box binding protein 1 / DB_XREF=gi:4827057 / UG=Hs.149923 X-box binding protein 1 / FL=gb:BC000938.1 gb:M31627.1 gb:NM_005080.1
211612_s_at	gb:U62858.1 / DEF=Human interleukin-13 receptor mRNA, complete cds. / FEA=mrna / PROD=interleukin-13 receptor / DB_XREF=gi:1695875 / FL=gb:U62858.1
203233_at	gb:NM_000418.1 / DEF=Homo sapiens interleukin 4 receptor (IL4R), mRNA. / FEA=mrna / GEN=IL4R / PROD=interleukin 4 receptor precursor / DB_XREF=gi:4557668 / UG=Hs.75545 interleukin 4 receptor / FL=gb:NM_000418.1
204507_s_at	gb:NM_000945.1 / DEF=Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I) (PPP3R1), mRNA. / FEA=mrna / GEN=PPP3R1 / PROD=protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I) / DB_XREF=gi:4506024 / UG=Hs.278540 protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I) / FL=gb:M30773.1 gb:NM_000945.1
218136_s_at	gb:NM_018579.1 / DEF=Homo sapiens mitochondrial solute carrier (LOC51312), mRNA. / FEA=mrna / GEN=LOC51312 / PROD=hypothetical protein PRO1278 / DB_XREF=gi:8924027 / UG=Hs.300496 mitochondrial solute carrier / FL=gb:AF155660.1 gb:AF116630.1
201582_at	Consensus includes gb:AL121900 / DEF=Human DNA sequence from clone RP11-379J5 on chromosome 20 Contains the last exon of the SEC23B gene for Sec23 (S. cerevisiae) homolog B, a putative novel gene, the 5' end of the gene for a novel protein similar to bacterial histidyl-tRNA synthetase... / FEA=mrna / DB_XREF=gi:11121203 / UG=Hs.173497 Sec23 (S. cerevisiae) homolog B / FL=gb:BC005404.1 gb:NM_006363.1
209339_at	gb:U76248.1 / DEF=Human hSIAH2 mRNA, complete cds. / FEA=mrna / PROD=hSIAH2 / DB_XREF=gi:2673967 / UG=Hs.20191 seven in absentia (Drosophila) homolog 2 / FL=gb:U76248.1 gb:NM_005067.1
208030_s_at	gb:NM_001119.2 / DEF=Homo sapiens adducin 1 (alpha) (ADD1), transcript variant 1, mRNA. / FEA=mrna / GEN=ADD1 / PROD=adducin 1 (alpha) isoform a / DB_XREF=gi:7710113 / FL=gb:NM_001119.2

201195_s_at	gb:AB018009.1 /DEF=Homo sapiens mRNA for L-type amino acid transporter 1, complete cds. /FEA=mRNA /GEN=HLAT1 /PROD=L-type amino acid transporter 1 /DB_XREF=gi:5926731 /UG=Hs.184601 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 /FL=gb:AF077866.1 gb:AB018542.1 gb:AF104032.1 gb:NM_003486.1 gb:AB017908.1 gb:AB018009.1 gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB_XREF=gi:7661821 /UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1 gb:AF161511.1 gb:NM_014183.1 gb:AF165516.1
217918_at	

55

Beschreibung der Sequenz in der Genebank Datenbank	
Affymetrix interne Bezeichnung	
221798_x_at	Consensus includes gb:AI183766 /FEA=EST /DB_XREF=gi:3734404 /DB_CLONE=IMAGE:1739290 /UG=Hs.182426 ribosomal protein S2
218231_at	gb:NM_017567.1 /DEF=Homo sapiens N-Acetylglucosamine kinase (HSA242910), mRNA. /FEA=mrna /GEN=HSA242910 /PROD=N-Acetylglucosamine kinase /DB_XREF=gi:8923736 /UG=Hs.7036 N-Acetylglucosamine kinase /FL=gb:BC001029.1 gb:BC005371.1 gb:NM_017567.1 Consensus includes gb:AI439556 /FEA=EST /DB_XREF=gi:4305149 /DB_XREF=est:tc90c12.x1 /CLONE=IMAGE:2073430 /UG=Hs.179526 upregulated by 1.25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1 gb:S73591.1 Consensus includes gb:AI583173 /FEA=EST /DB_XREF=gi:4569070 /DB_XREF=est:tg64e04.x1 /CLONE=IMAGE:2213598 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1
212998_x_at	Consensus includes gb:BG491844 /FEA=EST /DB_XREF=gi:13453356 /DB_XREF=est:602535931T1 /CLONE=IMAGE:4684998 /UG=Hs.78465 v-jun avian sarcoma virus 17 oncogene homolog /FL=gb:BC002646.1 gb:NM_002228.2 Consensus includes gb:AK026577.1 /DEF=Homo sapiens cdna: FLJ22924 fis, clone KAT06977, highly similar to HSALDAR Human fibroblast mRNA for aldolase A. /FEA=mrna /DB_XREF=gi:10439461 /UG=Hs.273415 aldolase A, fructose-bisphosphate
214687_x_at	gb:NM_014020.1 /DEF=Homo sapiens LR8 protein (LR8), mRNA. /FEA=mrna /GEN=LR8 /PROD=LR8 protein /DB_XREF=gi:7662497 /UG=Hs.190161
220532_s_at	LR8 protein /FL=gb:AF115384.1 gb:NM_014020.1 /UG=Hs.190161 /DEF=Homo sapiens CD1C antigen, c polypeptide (CD1C), mRNA. /FEA=mrna /GEN=CD1C /PROD=CD1C antigen, c polypeptide /
205987_at	gb:NM_001765.1 /DEF=Homo sapiens CD1C antigen, c polypeptide /FL=gb:M28827.1 gb:NM_001765.1 DB_XREF=gi:4502646 /UG=Hs.1311 CD1C antigen, c polypeptide /FL=gb:M28827.1 gb:NM_001765.1
202658_at	5.1 /DEF=Homo sapiens peroxisomal biogenesis factor 11B (PEX11B), mRNA. /FEA=mrna /GEN=PEX11B /PROD=peroxisomal biogenesis factor 11B /DB_XREF=gi:4505718 /UG=Hs.83023 peroxisomal biogenesis factor 11B /FL=gb:AF093670.1 gb:AB018080.1 gb:NM_003846.1
200991_s_at	gb:NM_014748.1 /DEF=Homo sapiens KIAA0064 gene product (KIAA0064), mRNA. /FEA=mrna /GEN=KIAA0064 /PROD=KIAA0064 gene product /
209007_s_at	DB_XREF=gi:7661889 /UG=Hs.278569 sorting nexin 17 /FL=gb:BC002524.1 gb:BC002610.1 gb:D31764.1 gb:NM_014748.1 gb:AF267856.1 /DEF=Homo sapiens HT033 mRNA, complete cds. /FEA=mrna /PROD=HT033 /DB_XREF=gi:12006038 /UG=Hs.8084 hypothetical protein
213969_x_at	dJ465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1 Consensus includes gb:BF683426 /FEA=EST /DB_XREF=gi:11968834 /DB_XREF=est:602139603F1 /CLONE=IMAGE:4300777 /UG=Hs.183698 Ribosomal protein L29
200094_s_at	Consensus includes gb:AI004246 /FEA=EST /DB_XREF=gi:3213756 /DB_XREF=est:ou03g06.x1 /CLONE=IMAGE:1625242 /UG=Hs.75309 Consensus includes gb:BC004954.1 /DEF=Homo sapiens, clone MGC:10897, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for eukaryotic translation elongation factor 2)
208929_x_at	gb:BC004954.1 /DEF=Homo sapiens, clone MGC:10897, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for eukaryotic translation elongation factor 2) /DB_XREF=gi:13436331 /UG=Hs.180842 ribosomal protein L13 /FL=gb:BC000851.1 gb:BC004954.1 gb:NM_000977.1

206170_at	gb:NM_000024.2 /DEF=Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), mRNA. /FEA=mrna /GEN=ADRB2 /PROD=adrenergic, beta-2-, receptor, surface /DB_XREF=gi:13162366 /UG=Hs.2551 adrenergic, beta-2-, receptor, surface /FL=gb:NM_000024.2 gb:M15169.1
212582_at	Consensus includes gb:AL049923.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564E2282 (from clone DKFZp564E2282). /FEA=mrna /DB_XREF=gi:4884169 /UG=Hs.109694 KIAA1451 protein
208630_at	Consensus includes gb:AL972144 /FEA=EST /DB_XREF=gi:5768970 /DB_XREF=est:wt63b03.x1 /CLONE=IMAGE:2492333 /UG=Hs.75860 hydroxyl-Coenzyme A dehydrogenase3-ketocetyl-Coenzyme A thiolaseenoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit /FL=gb:NM_000182.1 gb:DL6480.1 gb:U04627.1
214058_at	Consensus includes gb:M19720 /DEF=Human L-myc protein gene, complete cds /FEA=mrna_2 /DB_XREF=gi:188906 /UG=Hs.92137 v-myc avian myelocytomatosis viral oncogene homolog 1, lung carcinoma derived
201991_s_at	Consensus includes gb:BF223224 /FEA=EST /DB_XREF=gi:11130401 /DB_XREF=est:7q30g05.x1 /CLONE=IMAGE:3700017 /UG=Hs.149436 kinesin family member 5B /FL=gb:NM_004521.1
212179_at	Consensus includes gb:AW157501 /FEA=EST /DB_XREF=gi:6228902 /DB_XREF=est:au83a02.x1 /CLONE=IMAGE:2782826 /UG=Hs.18368 DKFZp564B0769 protein
210949_s_at	Consensus includes gb:AV700415 /FEA=EST /DB_XREF=gi:10302386 /DB_XREF=est:AV700415 /CLONE=GKODGA04 /UG=Hs.12969 hypo-MGC:8693, mRNA, complete cds. /FEA=mrna /PROD=Similar to eukaryotic translation initiation factor 3, subunit 8 (110kd) /DB_XREF=gi:12653522 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kd) /FL=gb:BC000533.1
213142_x_at	Consensus includes gb:AV700415 /FEA=EST /DB_XREF=gi:10302386 /DB_XREF=est:AV700415 /CLONE=GKODGA04 /UG=Hs.12969 hypo-MGC:8693, mRNA, complete cds. /FEA=mrna /PROD=Similar to eukaryotic translation initiation factor 3, subunit 8 (110kd), clone
217817_at	Consensus includes gb:BE891920 /FEA=EST /DB_XREF=gi:10351728 /DB_XREF=est:601435490F1 /CLONE=IMAGE:3920590 /UG=Hs.323342 actin related protein 23 complex, subunit 4 (20 kd) /FL=gb:AF006087.1 gb:NM_005718.1
216041_x_at	Consensus includes gb:223348.1 /DEF=Homo sapiens cDNA FLJ13286 fls, clone OVARC1001154, highly similar to Homo sapiens clone 24720 epithelin 1 and 2 mRNA. /FEA=mrna /DB_XREF=gi:10435243 /UG=Hs.180577 granulin
202687_s_at	gb:U57059.1 /DEF=Homo sapiens Apo-2 ligand mRNA, complete cds. /FEA=mrna /PROD=Apo-2 ligand /DB_XREF=gi:1336207 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 gb:NM_003810.1
215230_x_at	Consensus includes gb:AA679705 /FEA=EST /DB_XREF=gi:2660227 /DB_XREF=est:ah15e04.sl /CLONE=IMAGE:1156734 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kd)
200647_x_at	gb:NM_003752.2 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kd) (EIF3S8), mRNA. /FEA=mrna /GEN=EIF3S8 /PROD=eukaryotic translation initiation factor 3, subunit 8 (110kd) /DB_XREF=gi:5579457 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kd) /FL=gb:NM_003752.2
200078_s_at	gb:BC005876.1 /DEF=Homo sapiens, ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kd, clone MGC:4498, mRNA, complete cds. /FEA=mrna /PROD=ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kd /DB_XREF=gi:13543437 /FL=gb:BC005876.1
202169_s_at	gb:AF302110.1 /DEF=Homo sapiens alpha-aminoadipic semialdehyde dehydrogenase-phosphopantetheinyl transferase complete cds. /FEA=mrna /PROD=alpha-aminoadipic semialdehyde dehydrogenase-phosphopantetheinyl transferase /DB_XREF=gi:11120434 /UG=Hs.64595 aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase /FL=gb:AF302110.1 gb:AF136978.1 gb:AF151838.1 gb:AF151057.1 gb:NM_015423.1 gb:AF201943.1
202659_at	gb:NM_002801.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10), mRNA. /FEA=mrna /GEN=PSMB10 /PROD=proteasome (prosome, macropain) subunit, beta type, 10 /FL=gb:NM_002801.1
221488_s_at	gb:AF230924.1 /DEF=Homo sapiens brain acetylcholinesterase putative membrane anchor mRNA, complete cds. /FEA=mrna /PROD=brain acetylcholinesterase putative membrane anchor /DB_XREF=gi:7341254 /UG=Hs.107187 divalent cation tolerant protein CUTA /FL=gb:AF230924.1
221622_s_at	gb:AF246240.1 /DEF=Homo sapiens HT026 mRNA, complete cds. /FEA=mrna /PROD=HT026 /DB_XREF=gi:12005514 /UG=Hs.24371 uncharacterized hypothalamus protein HT007 /FL=gb:AF246240.1



	gb:NM_002939.1 /DEF=Homo sapiens ribonucleaseangiogenin inhibitor (RNH), mRNA. /FEA=mrna /GEN=RNH /PROD=ribonucleaseangiogenin
206050_s_at	inhibitor /DB_XREF=gi:4506564 /UG=Hs.75108 ribonucleaseangiogenin inhibitor /FL=gb:M36717.1 gb:NM_002939.1
212199_at	Consensus includes gb:AL566962 /FEA=EST /DB_XREF=gi:12919867 /DB_XREF=est:AL566962 /CLONE=CSDF026YH08 (3 prime) /UG=Hs.284281 Human putative ribosomal protein S1 mRNA
201861_s_at	Consensus includes gb:BF955566 /FEA=EST /DB_XREF=gi:12332781 /DB_XREF=est:602277032F1 /CLONE=IMAGE:4364790 /UG=Hs.326159 leucine rich repeat (in FLII) interacting protein 1 /FL=gb:NM_004735.1
212795_at	Consensus includes gb:AL137753.1 /DEF=Homo sapiens mRNA; cDNA DKFp434K1412 (from clone DKFp434K1412). /FEA=mrna /DB_XREF=gi:6808455 /UG=Hs.12144 KIAA1033 protein
213574_s_at	Consensus includes gb:AA861608 /FEA=EST /DB_XREF=gi:2953748 /DB_XREF=est:ak34e01.s1 /CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (importin) beta 1
215171_s_at	Consensus includes gb:AK023063.1 /DEF=Homo sapiens cDNA FLJ13001 fis, clone NT2RP3000341, highly similar to Homo sapiens mitochondrial inner membrane preprotein translocase Timl7a mRNA, nuclear gene encoding mitochondrial protein. /FEA=mrna /DB_XREF=gi:10434808 /UG=Hs.20716 translocase of inner mitochondrial membrane 17 (yeast) homolog A
210137_s_at	gb:BC001286.1 /DEF=Homo sapiens, similar to dCMP deaminase, clone MGC:5160, mRNA, complete cds. /FEA=mrna /PROD=Similar to dCMP deaminase /DB_XREF=gi:12654884 /UG=Hs.76894 dCMP deaminase /FL=gb:BC001286.1
212943_at	Consensus includes gb:AB011100.2 /DEF=Homo sapiens mRNA for KIAA0528 protein, partial cds. /FEA=mrna /GEN=KIAA0528 /PROD=KIAA0528 protein /DB_XREF=gi:6683714 /UG=Hs.30656 KIAA0528 gene product
202164_s_at	gb:AF180476.1 /DEF=Homo sapiens CALIFP (CALIF) mRNA, complete cds. /FEA=mrna /GEN=CALIF /PROD=CALIFP /DB_XREF=gi:6856208 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1
209005_at	gb:AF157323.1 /DEF=Homo sapiens p45SKP2-like protein mRNA, complete cds. /FEA=mrna /PROD=p45SKP2-like protein /DB_XREF=gi:7688696 /UG=Hs.5548 f-box and leucine-rich repeat protein 5 /FL=gb:AF199420.1 gb:AF142481.1 gb:AF157323.1
202899_s_at	gb:NM_003017.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 3 (SFRS3), mRNA. /FEA=mrna /GEN=SFRS3 /PROD=splicing factor, arginineserine-rich 3 /DB_XREF=gi:4506900 /UG=Hs.167460 splicing factor, arginineserine-rich 3 /FL=gb:L10838.1 gb:NM_003017.1
208777_s_at	gb:AF001212.1 /DEF=Homo sapiens 26S proteasome subunit 9 mRNA, complete cds. /FEA=mrna /PROD=26S proteasome subunit 9 /DB_XREF=gi:2150045 /UG=Hs.90744 proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 /FL=gb:BC000437.1 gb:BC004430.1 gb:AB003102.1 gb:AF001212.1 gb:NM_002815.1
219889_at	gb:NM_005479.1 /DEF=Homo sapiens frequently rearranged in advanced T-cell lymphomas (FRAT1), mRNA. /FEA=mrna /GEN=FRAT1 /PROD=frequently rearranged in advanced T-cell lymphomas /DB_XREF=gi:4885246 /UG=Hs.126057 frequently rearranged in advanced T-cell lymphomas /FL=gb:U59975.2 gb:NM_005479.1
204961_s_at	gb:NM_000265.1 /DEF=Homo sapiens neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) (NCF1), mRNA. /FEA=mrna /GEN=NCF1 /PROD=neutrophil cytosolic factor 1 /DB_XREF=gi:4557784 /UG=Hs.1583 neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) /FL=gb:BC002816.1 gb:AF330627.1 gb:M55067.1 gb:M25665.1 gb:NM_000265.1
217106_x_at	Consensus includes gb:AF091078.1 /DEF=Homo sapiens clone 559 unknown mRNA, complete sequence. /FEA=mrna /PROD=unknown /DB_XREF=gi:3859993 /UG=Hs.125819 putative dimethyladenosine transferase
212224_at	Consensus includes gb:NM_000689.1 /DEF=Homo sapiens aldehyde dehydrogenase 1, soluble (ALDH1), mRNA. /FEA=CDS /GEN=ALDH1 /PROD=aldehyde dehydrogenase 1, soluble /DB_XREF=gi:4502030 /UG=Hs.76392 aldehyde dehydrogenase 1 family, member A1 /FL=gb:AF003341.1 gb:NM_000689.1
204125_at	gb:NM_016013.1 /DEF=Homo sapiens CGI-65 protein (LOC511103), mRNA. /FEA=mrna /GEN=LOC511103 /PROD=CGI-65 protein /DB_XREF=gi:7705778 /UG=Hs.106529 CGI-65 protein /FL=gb:BC000780.1 gb:AF151823.1 gb:NM_016013.1
217752_s_at	gb:NM_018235.1 /DEF=Homo sapiens hypothetical protein FLJ10830 (FLJ10830), mRNA. /FEA=mrna /GEN=FLJ10830 /PROD=hypothetical protein
221087_s_at	FLJ10830 /DB_XREF=gi:8922698 /UG=Hs.273230 hypothetical protein FLJ10830 /FL=gb:BC001375.1 gb:BC003176.1 gb:NM_018235.1
	gb:NM_014349.1 /DEF=Homo sapiens apolipoprotein L, 3 (APO13), mRNA. /FEA=mrna /GEN=APO13 /PROD=apolipoprotein L, 3

	/DB_XREF=gi:7656972 /UG=Hs.241535 apolipoprotein L, 3 /FL=gb:AY014905.1 gb:AF070675.1 gb:NM_014349.1
	gb:NM_018229.1 /DEF=Homo sapiens hypothetical protein FLJ10813 (FLJ10813), mRNA. /FEA=mrna /GEN=FLJ10813 /PROD=hypothetical protein FLJ10813 /DB_XREF=gi:8922687 /UG=Hs.106210 hypothetical protein FLJ10813 /FL=gb:AL136685.1 gb:NM_018229.1
218139_s_at	Consensus includes gb:AI685944 /FEA=EST /DB_XREF=gi:4897238 /DB_XREF=est:tu38g02.x1 /CLONE=IMAGE:2253362 /UG=Hs.235069 RecQ protein-like (DNA helicase Q1-like)
213878_at	gb:NM_024551.1 /DEF=Homo sapiens hypothetical protein FLJ21432 (FLJ21432), mRNA. /FEA=mrna /GEN=FLJ21432 /PROD=hypothetical protein FLJ21432 /DB_XREF=gi:13375714 /UG=Hs.11641 hypothetical protein FLJ21432 /FL=gb:NM_024551.1 gb:BC004906.1
201346_at	Consensus includes gb:AL138761 /DEF=Human DNA sequence from clone RP11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha 1 (BP180), ESTs and GSSs. /FEA=mrna_2 /DB_XREF=gi:8573811 /UG=Hs.105751 Ste20-related serine/threonine kinase /FL=gb:D86959.1 gb:NM_014720.1
206874_s_at	Consensus includes gb:NM_004251.1 /DEF=Homo sapiens RAB9, member RAS oncogene family (RAB9), mRNA. /FEA=CDS /GEN=RAB9 /PROD=RAB9, member RAS oncogene family /DB_XREF=gi:4759011 /UG=Hs.28726 RAB9, member RAS oncogene family /FL=gb:U44103.1 gb:NM_004251.1
221808_at	gb:BC005297.1 /DEF=Homo sapiens, Similar to kynurenine 3-monooxygenase (kynurenine 3-hydroxylase), clone MGC:12362, mRNA, complete cds. /FEA=mrna /PROD=Similar to kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /DB_XREF=gi:13529016 /UG=Hs.107318 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /FL=gb:BC005297.1
211138_s_at	gb:AF279891.1 /DEF=Homo sapiens dead box protein 15 mRNA, complete cds. /FEA=mrna /PROD=dead box protein 15 /DB_XREF=gi:9624452 /UG=Hs.5683 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 15 /FL=gb:AB001636.1 gb:NM_001358.1 gb:AF279891.1
201386_s_at	gb:NM_014751.1 /DEF=Homo sapiens KIAA0429 gene product (KIAA0429), mRNA. /FEA=mrna /GEN=KIAA0429 /PROD=KIAA0429 gene product
203037_s_at	/DB_XREF=gi:7662113 /UG=Hs.77694 KIAA0429 gene product /FL=gb:AB007889.1 gb:NM_014751.1
218356_at	gb:NM_013393.1 /DEF=Homo sapiens cell division protein FtsJ (FtsJ), mRNA. /FEA=mrna /GEN=FtsJ /PROD=cell division protein FtsJ /DB_XREF=gi:7019376 /UG=Hs.279877 cell division protein FtsJ /FL=gb:AF093415.1 gb:NM_013393.1
204405_x_at	gb:NM_014473.1 /DEF=Homo sapiens putative dimethyladenosine transferase (HSA9761), mRNA. /FEA=mrna /GEN=HSA9761 /PROD=putative dimethyladenosine transferase /DB_XREF=gi:7657197 /UG=Hs.125819 putative dimethyladenosine transferase /FL=gb:AF102147.1 gb:NM_014473.1
	gb:NM_007062.1 /DEF=Homo sapiens nuclear phosphoprotein similar to S. cerevisiae PWP1 (PWP1), mRNA. /FEA=mrna /GEN=PWP1 /PROD=nuclear phosphoprotein similar to S. cerevisiae PWP1 /DB_XREF=gi:5902033
201608_s_at	/UG=Hs.172589 nuclear phosphoprotein similar to S. cerevisiae PWP1 /FL=gb:BC001652.1 gb:L07758.1 gb:NM_007062.1 gb:NM_015380.1 /DEF=Homo sapiens CGI-51 protein (CGI-51), mRNA. /FEA=mrna /GEN=CGI-51 /PROD=CGI-51 protein /DB_XREF=gi:7661541
201569_s_at	/UG=Hs.4877 CGI-51 protein /FL=gb:AF151809.1 gb:NM_015380.1
222244_s_at	Consensus includes gb:AK000749.1 /DEF=Homo sapiens cDNA FLJ20742 fls, clone HEP06891. /FEA=mrna /DB_XREF=gi:7021031 /UG=Hs.52184 hypothetical protein FLJ20618
	gb:NM_004939.1 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 (DDX1), mRNA. /FEA=mrna /GEN=DDX1 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 /DB_XREF=gi:4826685 /UG=Hs.78580 DEADH (Asp-Glu-Ala-AspHis) box pol- ypeptide 1
201241_at	/FL=gb:X70649.1 gb:NM_004939.1
220731_s_at	gb:NM_018090.1 /DEF=Homo sapiens hypothetical protein FLJ10420 (FLJ10420), mRNA. /FEA=mrna /GEN=FLJ10420 /PROD=hypothetical protein FLJ10420 /DB_XREF=gi:8922415 /UG=Hs.289087 hypothetical protein FLJ10420 /FL=gb:NM_018090.1 gb:BC004146.1 /DEF=Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 5, clone MGC:2175, mRNA, complete cds.
208799_at	

	/FEA-mRNA /PROD=proteasome (prosome, macropain) subunit, betatype, 5 /DB_XREF=gi:13278740 /UG=Hs.78596 proteasome (prosome, macropain) subunit, beta type, 5 /FL=gb:BC004146.1 gb:NM_002797.1 gb:D29011.1
221718_s_at	gb:NM030360.1 /DEF=Human type II cAMP-dependent protein kinase (HC31) mRNA, complete cds. /FEA=CDS /GEN=Ht31 /PROD=protein_kinase /DB_XREF=gi:184434 /FL=gb:M90360.1
208662_s_at	Consensus includes gb:AI885338 /FEA=EST /DB_XREF=gi:5590502 /DB_XREF=est:w192e09.x1 /CLONE=IMAGE:2432392 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:D84294.1
202118_s_at	Consensus includes gb:AA541758 /FEA=EST /DB_XREF=gi:2288192 /DB_XREF=est:ni87d05.s1 /CLONE=IMAGE:983817 /UG=Hs.14158 copine III /FL=gb:AB014536.1 gb:NM_003909.1 gb:AF077226.2
	gb:NM_004551.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) (NDUFS3), mRNA. /FEA=mRNA /GEN=NDUFS3 /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)
201740_at	/DB_XREF=gi:4758787 /UG=Hs.5273 NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) /FL=gb:BC000617.1 gb:AF067139.1 gb:NM_004551.1 gb:AF100743.1
215952_s_at	Consensus includes gb:AF090094.1 /DEF=Homo sapiens clone IMAGE 172979. /FEA=mRNA /DB_XREF=gi:4063629 /UG=Hs.125078 ornithine decarboxylase antizyme 1
212796_s_at	Consensus includes gb:BF195608 /FEA=EST /DB_XREF=gi:11082676 /DB_XREF=est:7n85f03.x1 /CLONE=IMAGE:3571349 /UG=Hs.126084 KIAA1055 protein
	gb:AL110243.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564B0482 (from clone DKFZp564B0482); complete cds. /FEA=mRNA /GEN=DKFZp564B0482 /PROD=hypothetical protein /DB_XREF=gi:5817189 /UG=Hs.187991 DKFZp564A122 protein
210561_s_at	/FL=gb:AF072880.1 gb:AF106683.1 gb:AL110243.1 gb:AF112205.1 gb:AF069313.2
202220_at	gb:NM_014949.1 /DEF=Homo sapiens KIAA0907 protein (KIAA0907), mRNA. /FEA=mRNA /GEN=KIAA0907 /PROD=KIAA0907 protein /DB_XREF=gi:7662371 /UG=Hs.24656 KIAA0907 protein /FL=gb:AB020714.1 gb:NM_014949.1
	gb:NM_006526.1 /DEF=Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /FEA=mRNA /GEN=ZNF217 /PROD=zinc finger protein 217
203739_at	/DB_XREF=gi:5730123 /UG=Hs.155040 zinc finger protein 217 /FL=gb:AF041259.1 gb:NM_005526.1
211036_x_at	gb:BC006301.1 /DEF=Homo sapiens, anaphase-promoting complex subunit 5, clone MGC:13295, mRNA, complete cds. /FEA=mRNA /PROD=anaphase-promoting complex subunit 5 /DB_XREF=gi:13623410 /FL=gb:BC006301.1
	gb:NM_005044.1 /DEF=Homo sapiens protein kinase, X-linked (PRKX), mRNA. /FEA=mRNA /GEN=PRKX /PROD=protein kinase, X-linked
204060_s_at	/DB_XREF=gi:4826947 /UG=Hs.147996 protein kinase, X-linked /FL=gb:NM_005044.1
64064_at	Cluster Incl. AI435089:th95b11.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2126397 /clone_end=3 /gb=AI435089 /gi=4300737 /ug=Hs.26194 /len=891
201515_s_at	gb:NM_004622.1 /DEF=Homo sapiens translin (TSN), mRNA. /FEA=mRNA /GEN=TSN /PROD=translin /DB_XREF=gi:4759259 /UG=Hs.75066 translin /FL=gb:NM_004622.1
219093_at	gb:NM_017933.1 /DEF=Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /FEA=mRNA /GEN=FLJ20701 /PROD=hypothetical protein FLJ20701 /DB_XREF=gi:8923631 /UG=Hs.169764 hypothetical protein FLJ20701 /FL=gb:NM_017933.1
221739_at	Consensus includes gb:AL524093 /FEA=EST /DB_XREF=gi:12787586 /DB_XREF=est:AL524093 /CLONE=CS0DC002YI04 (5 prime) /UG=Hs.10927 hypothetical protein EUROIMAGE1875335
208822_s_at	gb:U18321.1 /DEF=Human ionizing radiation resistance conferring protein mRNA, complete cds. /FEA=mRNA /PROD=ionizing radiation resistance conferring protein /DB_XREF=gi:603763 /UG=Hs.159627 death associated protein 3 /FL=gb:U18321.1
	gb:NM_014222.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) (NDUFAB1), mRNA. /FEA=mRNA /GEN=NDUFAB1 /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) /DB_XREF=gi:7657368
218160_at	/UG=Hs.31547 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) /FL=gb:BC001016.1 gb:AF044953.1 gb:NM_014222.1
221728_x_at	Consensus includes gb:AA628440 /FEA=EST /DB_XREF=gi:2540827 /DB_XREF=est:af26f02.s1 /CLONE=IMAGE:1032795 /UG=Hs.83623 nuclear receptor subfamily 1, group I, member 3

210943_s_at	gb:U84744.1 / DEF=Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds. / FE=mrna / GEN=LYST / PROD=Chediak-Higashi syndrome protein short isoform / DB_XREF=gi:2654473 / UG=Hs.36508 Chediak-Higashi syndrome 1 / FL=gb:U84744.1
210943_s_at	gb:BC000009.1 / DEF=Homo sapiens, likely homolog of yeast Mhp2, component of the HACA snRNP; hypothetical protein FLJ20479, clone MGC:1038, mRNA, complete cds. / FE=mrna / PROD=likely homolog of yeast Mhp2, component of the HACA snRNP; hypothetical protein FLJ20479 / DB_XREF=gi:12652540 / UG=Hs.23990 nucleolar protein family A, member 2 (HACA small nucleolar RNPs) / FL=gb:BC000009.1 gb:NM_017838.1
209104_s_at	gb:NM_019048.1 / DEF=Homo sapiens hypothetical protein (FLJ20752), mRNA. / FE=mrna / GEN=hypothetical protein tein / DB_XREF=gi:9506696 / UG=Hs.101364 hypothetical protein / FL=gb:BC001243.1 gb:NM_019048.1
217987_at	gb:NM_002806.1 / DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6), mRNA. / FE=mrna / GEN=PSMC6 / PROD=proteasome (prosome, macropain) 26S subunit, ATPase, 6 / DB_XREF=gi:4506214 / UG=Hs.79357 proteasome (prosome, macropain) 26S subunit, ATPase, 6 / FL=gb:BC005390.1 gb:AF006305.1 gb:NM_002806.1
201699_at	gb:NM_016451.1 / DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. / FE=mrna / GEN=COPB / PROD=coatomer protein complex, subunit beta / DB_XREF=gi:7705368 / UG=Hs.3059 coatomer protein complex, subunit beta / FL=gb:AF084457.1 gb:AL136593.1 gb:NM_016451.1
201359_at	gb:M80261.1 / DEF=Human apurinic endonuclease (APE) mRNA, complete cds. / FE=mrna / GEN=APE / PROD=apurinic endonuclease / DB_XREF=gi:178742 / UG=Hs.73722 APEX nuclease (multifunctional DNA repair enzyme) / FL=gb:BC004979.1 gb:M80261.1
210027_s_at	gb:NM_000714.2 / DEF=Homo sapiens benzodiazepine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA. / FE=mrna / GEN=BZRP / PROD=peripheral benzodiazepine receptor / DB_XREF=gi:6382068 / UG=Hs.202 benzodiazepine receptor (peripheral) / FL=gb:BC001110.1 gb:M36035.1 gb:NM_000714.2
202096_s_at	Consensus includes gb:AL050136.1 / DEF=Homo sapiens mRNA; cDNA DKFp586L141 (from clone DKFp586L141). / FE=mrna / DB_XREF=gi:4884346 / UG=Hs.140945 Homo sapiens mRNA; cDNA DKFp586L141 (from clone DKFp586L141)
214948_s_at	gb:NM_014306.1 / DEF=Homo sapiens hypothetical protein (HSPC117), mRNA. / FE=mrna / GEN=HSPC117 / PROD=similar to C. elegans hypothetical 55.2 kD protein FL6A11.2 / DB_XREF=gi:7657014 / UG=Hs.10729 hypothetical protein
200042_at	FL=gb:BC000151.1 gb:BC002970.1 gb:AF161466.1 gb:NM_014306.1 gb:AF155658.1
219035_s_at	gb:NM_025126.1 / DEF=Homo sapiens hypothetical protein FLJ21786 (FLJ21786), mRNA. / FE=mrna / GEN=FLJ21786 / PROD=hypothetical protein FLJ21786 / DB_XREF=gi:13376704 / UG=Hs.316809 hypothetical protein FLJ21786 / FL=gb:NM_025126.1
200041_s_at	gb:NM_004640.1 / DEF=Homo sapiens HLA-B associated transcript-1 (D6S81E), mRNA. / FE=mrna / GEN=D6S81E / PROD=HLA-B associated transcript-1 / DB_XREF=gi:4758111 / UG=Hs.55296 HLA-B associated transcript-1 / FL=gb:BC004350.1 gb:NM_004640.1
216321_s_at	Consensus includes gb:X03348.1 / DEF=Human mRNA for beta-glucocorticoid receptor (clone OB10). / FE=mrna / PROD=beta-glucocorticoid receptor / DB_XREF=gi:31681 / UG=Hs.75772 nuclear receptor subfamily 3, group C, member 1
214574_x_at	Consensus includes gb:NM_007161.1 / DEF=Homo sapiens DNA segment on chromosome 6 (unique) 49 expressed sequence, NK cell triggering receptor, p30 (D6S49E), mRNA. / FE=CDS / GEN=D6S49E / PROD=leukocyte-specific transcript 1 / DB_XREF=gi:6005740 / UG=Hs.89411 lymphocyte antigen 117 / FL=gb:NM_007161.1
205370_x_at	gb:NM_001918.1 / DEF=Homo sapiens dihydropyrimidine branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT), mRNA. / FE=mrna / GEN=DBT / PROD=dihydropyrimidine branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) / FL=gb:J03208.1 gb:NM_001918.1 gb:M27093.1
213872_at	Consensus includes gb:BE45032 / FE=EST / DB_XREF=gi:9510807 / DB_XREF=est:hv76g09.x1 / CLONE=IMAGE:3179392

	UG-Hs.173685 hypothetical protein FLJ12619	
201576_s_at	gb:NM_000404.1 /DEF=Homo sapiens galactosidase, beta 1 (GLB1), mRNA. /FEA=mrna /GEN=GLB1 /PROD=galactosidase, beta 1 /DB_XREF=gi:10834965 /UG=Hs.79222 galactosidase, beta 1 /FL=gb:NM_000404.1 gb:M27507.1 gb:M22590.1 gb:M34423.1 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SSP), mRNA. /FEA=mrna /GEN=P85SSP /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1	
202548_s_at	gb:NM_012197.2 /DEF=Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA. /FEA=mrna /GEN=GAPCENA /PROD=rab6 GTPase activating protein (GAP and centrosome-associated) /DB_XREF=gi:12323372 /UG=Hs.55099 rab6 GTPase activating protein (GAP and centrosome-associated) /FL=gb:NM_012197.2 Consensus includes gb:AUI54504 /FEA=EST /DB_XREF=gi:11016025 /DB_XREF=est:AUI54504 /CLONE=NT2RP4001328 /UG=Hs.154654 cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM_000104.2 gb:U03688.1	
202435_s_at	gb:NM_017840.1 /DEF=Homo sapiens hypothetical protein FLJ20484 (FLJ20484), mRNA. /FEA=mrna /GEN=FLJ20484 /PROD=hypothetical protein FLJ20484 /DB_XREF=gi:8923447 /UG=Hs.5080 hypothetical protein FLJ20484 /FL=gb:AF275806.1 gb:BC001040.1 gb:NM_017840.1 gb:AF183428.1	
217980_s_at	gb:NM_001316.1 /DEF=Homo sapiens chromosome segregation 1 (yeast homolog)-like /DB_XREF=gi:4503072 /UG=Hs.90073 chromosome segregation 1 /GEN=CSE1L /PROD=chromosome segregation 1 (yeast homolog)-like /DB_XREF=gi:4503072 /UG=Hs.90073 chromosome segregation 1 (yeast homolog)-like /FL=gb:U03286.1 gb:AF053641.1 gb:NM_001316.1	
201112_s_at	gb:NM_004837.1 /DEF=Homo sapiens geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA. /FEA=mrna /GEN=GGPS1 /PROD=geranylgeranyl diphosphate synthase 1 /DB_XREF=gi:4758429 /UG=Hs.55498 geranylgeranyl diphosphate synthase 1 /FL=gb:AF057698.1 gb:BC005252.1 gb:AB017971.1 gb:AB016043.1 gb:AB019036.1 gb:NM_004837.1 gb:AF125394.1	
202322_s_at	gb:NM_024079.1 /DEF=Homo sapiens hypothetical protein MGC2840 similar to a putative glucosyltransferase (MGC2840), mRNA. /FEA=mrna /GEN=MGC2840 /PROD=hypothetical protein MGC2840 similar to a putative glucosyltransferase /DB_XREF=gi:13129069 /UG=Hs.155356 hypothetical protein MGC2840 similar to a putative glucosyltransferase /FL=gb:BC001133.1 gb:NM_024079.1 Consensus includes gb:D42043.1 /DEF=Human mRNA for KIAA0084 gene, partial cds. /FEA=mrna /GEN=KIAA0084 /DB_XREF=gi:577298 /UG=Hs.79123 KIAA0084 protein	
212646_at	Consensus includes gb:AA887480 /FEA=EST /DB_XREF=gi:3003168 /DB_XREF=est:oj54a12.s1 /CLONE=IMAGE:1502110 /UG=Hs.17428 RBP1-like protein	
212591_at	Consensus includes gb:AA744771 /FEA=EST /DB_XREF=gi:2783535 /DB_XREF=est:ny71d07.s1 /CLONE=IMAGE:1283725 /UG=Hs.108642 zinc finger protein 22 (KOX 15) /FL=gb:NM_006963.1	
218005_at	Consensus includes gb:BE670915 /FEA=EST /DB_XREF=gi:10031456 /DB_XREF=est:7e43a09.x1 /CLONE=IMAGE:3285208 /UG=Hs.153834 pumilio (Drosophila) homolog 1 /FL=gb:AF315592.1 gb:NM_014676.1	
201165_s_at	Consensus includes gb:AI680192 /FEA=EST /DB_XREF=gi:4890374 /DB_XREF=est:tw66a10.x1 /CLONE=IMAGE:2264634 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
212239_at	Consensus includes gb:BF303597 /FEA=EST /DB_XREF=gi:11250218 /DB_XREF=est:tw66a10.x1 /CLONE=IMAGE:2264634 /UG=Hs.182695 hypothetical protein MGC3243 /FL=gb:BC000002.1 gb:NM_024076.1	
204386_s_at	Consensus includes gb:AI091079 /FEA=EST /DB_XREF=gi:3430138 /DB_XREF=est:qa53e05.s1 /CLONE=IMAGE:1690496 /UG=Hs.81972 SHC (Src homology 2 domain-containing) transforming protein 1	
214853_s_at	gb:I25275.1 /DEF=Human estrogen sulfotransferase mRNA, complete cds. /FEA=mrna /PROD=estrogen sulfotransferase /DB_XREF=gi:463124 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /FL=gb:L25275.1 /DB_XREF=gi:463124 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /FL=gb:L25275.1 Consensus includes gb:AK026747.1 /DEF=Homo sapiens cDNA: FLJ23094 f1s, clone LING07379, highly similar to HST000007 Homo sapiens	
210580_x_at	Consensus includes gb:AK026747.1 /DEF=Homo sapiens cDNA: FLJ23094 f1s, clone LING07379, highly similar to HST000007 Homo sapiens	
222150_s_at	mRNA full length insert cDNA clone EUROIMAGE 293605. /FEA=mrna /DB_XREF=gi:10439670 /UG=Hs.12969 hypothetical protein gb:BC001650.1 /DEF=Homo sapiens, Similar to putative methyltransferase, clone MGC:2708, mRNA, complete cds. /FEA=mrna /PROD=Similar to putative methyltransferase /DB_XREF=gi:12804482 /UG=Hs.268149 putative methyltransferase /FL=gb:BC003031.1 gb:BC001650.1 gb:NM_019852.1	
209265_s_at		

	gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mrna /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390
218807_at	/UG=Hs.267659 vav 3 oncogene /FL=gb:AF067817.1 gb:AF118887.1 gb:NM_006113.2 /UG=Hs.267659 vav 3 oncogene /FL=gb:AF067817.1 gb:AF118887.1 gb:NM_006113.2 /FEA=mrna /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390
209043_at	gb:AF033026.1 /DEF=Homo sapiens bifunctional ATP sulfurylaseadenosine 5-phosphosulfate kinase /DB_XREF=gi:3378100 /FEA=mrna /PROD=bifunctional ATP sulfurylaseadenosine 5-phosphosulfate kinase /DB_XREF=gi:3378100 /UG=Hs.3833 3-phosphoadenosine 5-phosphosulfate synthase 1 /FL=gb:AF033026.1 gb:AF016496.1 gb:NM_005443.1 gb:AF105227.1 /FEA=mrna /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390
219777_at	gb:NM_024711.1 /DEF=Homo sapiens hypothetical protein FLJ22690 (FLJ22690), mRNA. /FEA=mrna /GEN=FLJ22690 /PROD=hypothetical protein FLJ22690 /DB_XREF=gi:13376008 /UG=Hs.105468 hypothetical protein FLJ22690 /FL=gb:NM_024711.1 /FEA=mrna /GEN=FLJ22690
218048_at	gb:NM_012071.1 /DEF=Homo sapiens BUP protein (BUP), mRNA. /FEA=mrna /GEN=BUP /PROD=BUP protein /DB_XREF=gi:6912277 /UG=Hs.35660 BUP protein /FL=gb:AF078848.1 gb:AF201948.1 gb:NM_012071.1 /FEA=mrna /GEN=BUP
201986_at	Consensus includes gb:AB011165.1 /DEF=Homo sapiens mRNA for KIAA0593 protein, partial cds. /FEA=mrna /GEN=KIAA0593 /PROD=KIAA0593 protein /DB_XREF=gi:3043709 /UG=Hs.11861 thyroid hormone receptor-associated protein, 240 kba subunit /FL=gb:AF117754.1 gb:NM_005121.1 /FEA=mrna /GEN=KIAA0593
219799_s_at	gb:NM_005771.1 /DEF=Homo sapiens retinol dehydrogenase homolog (RDHL), mRNA. /FEA=mrna /GEN=RDHL /PROD=retinol dehydrogenase homolog /DB_XREF=gi:5032034 /UG=Hs.179608 retinol dehydrogenase homolog /FL=gb:AF067174.1 /FEA=mrna /GEN=RDHL
208688_x_at	gb:NM_005771.1 /DEF=Homo sapiens eukaryotic translation initiation factor (eIF3) mRNA, complete cds. /FEA=mrna /GEN=eIF3 /PROD=eukaryotic translation initiation factor /DB_XREF=gi:2558667 /UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:U78525.1 /FEA=mrna /GEN=eIF3
200001_at	gb:NM_001749.1 /DEF=Homo sapiens calpain 4, small subunit (30K) (CAPN4), mRNA. /FEA=mrna /GEN=CAPN4 /PROD=calpain 4 small subunit /DB_XREF=gi:4502564 /UG=Hs.74451 calpain 4, small subunit (30K) /FL=gb:BC000592.1 gb:NM_001749.1 /FEA=mrna /GEN=CAPN4
218118_s_at	gb:NM_006327.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 23 (yeast) homolog (TIM23), mRNA. /FEA=mrna /GEN=TIM23 /PROD=translocase of inner mitochondrial membrane 23 (yeast) homolog /DB_XREF=gi:5454121 /UG=Hs.283684 translocase of inner mitochondrial membrane 23 (yeast) homolog /FL=gb:AF030162.1 gb:NM_006327.1 /FEA=mrna /GEN=TIM23
201840_at	gb:NM_006156.1 /DEF=Homo sapiens neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA. /FEA=mrna /GEN=NEDD8 /PROD=neural precursor cell expressed, developmentally down-regulated 8 /DB_XREF=gi:5453759 /UG=Hs.75512 neural precursor cell expressed, developmentally down-regulated 8 /FL=gb:D23662.1 gb:NM_006156.1 /FEA=mrna /GEN=NEDD8
38710_at	Cluster Incl. AL096714:Homo sapiens mRNA; cDNA DKFp564E242 (from clone DKFp564E242) /cds=UNKNOWN /gb=AL096714 /gi=5419847 /ug=Hs.108504 /len=1904 /FEA=mrna /GEN=UNKNOWN
212287_at	Consensus includes gb:BF382924 /FEA=EST /DB_XREF=gi:11364313 /DB_XREF=est:601816985F1 /CLONE=IMAGE:4050909 /UG=Hs.197803 KIAA0160 protein /FEA=mrna /GEN=KIAA0160
203098_at	Consensus includes gb:AL050164.1 /DEF=Homo sapiens mRNA; cDNA DKFp586C1622 (from clone DKFp586C1622); partial cds. /FEA=mrna /GEN=DKFp586C1622 /PROD=hypothetical protein /DB_XREF=gi:4884378 /UG=Hs.16081 chromodomain protein, y chromosome-like /FL=gb:AF081259.1 gb:NM_004824.1 /FEA=mrna /GEN=DKFp586C1622
218905_at	gb:NM_017864.1 /DEF=Homo sapiens hypothetical protein FLJ20530 (FLJ20530), mRNA. /FEA=mrna /GEN=FLJ20530 /PROD=hypothetical protein FLJ20530 /DB_XREF=gi:8923495 /UG=Hs.279521 hypothetical protein FLJ20530 /FL=gb:NM_017864.1 /FEA=mrna /GEN=FLJ20530
218303_x_at	gb:NM_016618.1 /DEF=Homo sapiens hypothetical protein (LOC51315), mRNA. /FEA=mrna /GEN=LOC51315 /PROD=hypothetical protein /DB_XREF=gi:7706155 /UG=Hs.5721 hypothetical protein (LOC51315), mRNA. /FEA=mrna /GEN=LOC51315
208705_s_at	Consensus includes gb:BG481972 /FEA=EST /DB_XREF=gi:13414251 /DB_XREF=est:602526894F1 /CLONE=IMAGE:4650408 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1 /FEA=mrna /GEN=HCA66
218715_at	gb:NM_018428.1 /DEF=Homo sapiens hepatocellular carcinoma-associated antigen 66 (HCA66), mRNA. /FEA=mrna /GEN=HCA66 /PROD=hepatocellular carcinoma-associated antigen 66 /DB_XREF=gi:8923721 /UG=Hs.30670 hepatocellular carcinoma-associated antigen 66 /FL=gb:AF244135.1 gb:AF116631.1 gb:NM_018428.1 /FEA=mrna /GEN=HCA66
202184_s_at	gb:NM_018230.1 /DEF=Homo sapiens hypothetical protein FLJ10814 (FLJ10814), mRNA. /FEA=mrna /GEN=FLJ10814 /PROD=hypothetical protein FLJ10814 (FLJ10814), mRNA. /FEA=mrna /GEN=FLJ10814

202004_x_at	/PROD=hypothetical protein FLJ10814 /DB_XREF=gi:8922689 /UG=Hs.12457 hypothetical protein FLJ10814 /FL=gb:NM_018230.1
209435_s_at	gb:NM_003001.2 /DEF=Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=SDHC /PROD=succinate dehydrogenase complex, subunit C precursor /DB_XREF=gi:9257243 /UG=Hs.3577 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD /FL=gb:U57877.1 gb:NM_003001.2
209435_s_at	gb:BC000265.1 /DEF=Homo sapiens, clone MGC:3182, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:3182) /DB_XREF=gi:12653008 /UG=Hs.315417 Homo sapiens, clone MGC:3182, mRNA, complete cds /FL=gb:BC000265.1
221044_s_at	gb:NM_021616.1 /DEF=Homo sapiens ring finger protein 21, interferon-responsive (RNF21), mRNA. /FEA=mrna /GEN=RNF21 /PROD=ring finger protein 21, interferon-responsive /DB_XREF=gi:11055977 /UG=Hs.125300 ring finger protein 21, interferon-responsive /FL=gb:AB039903.1 gb:NM_021616.1
200992_at	Consensus includes gb:AL137335.1 /DEF=Homo sapiens mRNA; cDNA DKFp434A179 (from clone DKFp434A179); partial cds. /FEA=mrna /GEN=DKFp434A179 /PROD=hypothetical protein /DB_XREF=gi:6807827 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1
201900_s_at	gb:NM_006066.1 /DEF=Homo sapiens aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1), mRNA. /FEA=mrna /GEN=AKR1A1 /PROD=aldo-keto reductase family 1, member A1 (aldehyde reductase) /DB_XREF=gi:5174390 /UG=Hs.89529 aldo-keto reductase family 1, member A1 (aldehyde reductase) /FL=gb:BC000670.1 gb:J04794.1 gb:NM_006066.1
202560_s_at	gb:NM_015607.1 /DEF=Homo sapiens DKFp547E1010 protein (DKFp547E1010), mRNA. /FEA=mrna /GEN=DKFp547E1010 /PROD=DKFp547E1010 protein /DB_XREF=gi:7661589 /UG=Hs.323817 DKFp547E1010 protein /FL=gb:NM_015607.1
201105_at	gb:NM_002305.2 /DEF=Homo sapiens lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA. /FEA=mrna /GEN=LGALS1 /PROD=beta-galactosidase binding lectin precursor /DB_XREF=gi:6006015 /UG=Hs.227751 lectin, galactoside-binding, soluble, 1 (galectin 1) /FL=gb:BC001693.1 gb:J04456.1 gb:NM_002305.2
204546_at	gb:NM_014732.1 /DEF=Homo sapiens KIAA0513 gene product (KIAA0513), mRNA. /FEA=mrna /GEN=KIAA0513 /PROD=KIAA0513 gene product /DB_XREF=gi:7662163 /UG=Hs.301658 KIAA0513 gene product /FL=gb:AB011085.1 gb:NM_014732.1
214181_x_at	Consensus includes gb:AI735692 /FEA=EST /DB_XREF=gi:5057216 /DB_XREF=est:at20b12.x1 /CLONE=IMAGE:2355647 /UG=Hs.88411 lymphocyte antigen 1.17
219032_x_at	gb:NM_014322.1 /DEF=Homo sapiens opsin 3 (encephalopsin) (OPN3), mRNA. /FEA=mrna /GEN=OPN3 /PROD=opsin 3 (encephalopsin) /DB_XREF=gi:7657070 /UG=Hs.279926 opsin 3 (encephalopsin) /FL=gb:AF140242.1 gb:NM_014322.1
205306_x_at	Consensus includes gb:AI074145 /FEA=EST /DB_XREF=gi:3400789 /DB_XREF=est:ovl3a06.x1 /CLONE=IMAGE:1637170 /UG=Hs.107318 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /FL=gb:AF056032.1 gb:NM_003679.1
202837_at	gb:NM_006700.1 /DEF=Homo sapiens FLN29 gene product (FLN29), mRNA. /FEA=mrna /GEN=FLN29 /PROD=FLN29 gene product /DB_XREF=gi:5729827 /UG=Hs.5148 FLN29 gene product /FL=gb:BC003553.1 gb:AB007447.1 gb:NM_006700.1
202153_s_at	gb:NM_016553.1 /DEF=Homo sapiens hypothetical protein (DKFp547L134), mRNA. /FEA=mrna /GEN=DKFp547L134 /PROD=hypothetical protein /DB_XREF=gi:7705354 /UG=Hs.9877 hypothetical protein /FL=gb:AL162061.1 gb:NM_016553.1
209341_s_at	Consensus includes gb:AU153366 /FEA=EST /DB_XREF=gi:11014887 /DB_XREF=est:AU153366 /CLONE=VT2R3002988 /UG=Hs.226573 /inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta /FL=gb:AF031416.1 gb:AF080158.1
212493_s_at	Consensus includes gb:AI761110 /FEA=EST /DB_XREF=gi:5176777 /DB_XREF=est:w169h02.x1 /CLONE=IMAGE:2398611 /UG=Hs.6947 HSPC069 protein
201600_at	gb:NM_007273.1 /DEF=Homo sapiens B-cell associated protein (BEA), mRNA. /FEA=mrna /GEN=BEA /PROD=B-cell associated protein /DB_XREF=gi:6005853 /UG=Hs.7771 B-cell associated protein /FL=gb:AF150962.1 gb:NM_007273.1 gb:AF126021.1
201144_s_at	gb:NM_004094.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) (EIF2S1), mRNA. /FEA=mrna /GEN=EIF2S1 /PROD=eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) /DB_XREF=gi:4758255 /UG=Hs.151777 eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) /FL=gb:BC002513.1 gb:J02645.1
211985_s_at	Consensus includes gb:AI653730 /FEA=EST /DB_XREF=gi:4737709 /DB_XREF=est:wb36f12.x1 /CLONE=IMAGE:2307791 /UG=Hs.279009 matrix Gla protein



	gb:NM_005004.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8), mRNA. /FEA=mrna /GEN=NDUFB8 /PROD=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) /DB_XREF=gi:4826853
201226_at	/UG=Hs.198273 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) /FL=gb:BC000466.1 gb:AF044958.1 gb:AF077028.1 gb:NM_005004.1 gb:AL080056.1
	gb:BC004170.1 /DEF=Homo sapiens, histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit, clone MGC:2725, mRNA, complete cds. /FEA=mrna /PROD=histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit /DB_XREF=gi:13278800
	/UG=Hs.108112 histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit /FL=gb:BC003166.1 gb:BC004170.1
208828_at	gb:AF226077.1 gb:NM_017443.1
	Consensus includes gb:BF739943 /FEA=EST /DB_XREF=gi:12066607 /DB_XREF=est:70411504.x1 /CLONE=IMAGE:3576534
204020_at	/UG=Hs.29117 purine-rich element binding protein A /FL=gb:M96684.1 gb:NM_005859.1
	gb:NM_021821.1 /DEF=Homo sapiens MDS023 protein (MDS023), mRNA. /FEA=mrna /GEN=MDS023 /PROD=MDS023 protein
217942_at	/DB_XREF=gi:11141894 /UG=Hs.10724 MDS023 protein /FL=gb:AF182422.1 gb:NM_021821.1
	Consensus includes gb:BF971923 /FEA=EST /DB_XREF=gi:12339138 /DB_XREF=est:602240326F1 /CLONE=IMAGE:4328791
203514_at	/UG=Hs.29282 mitogen-activated protein kinase kinase 3 /FL=gb:U78876.1 gb:NM_002401.1
	Consensus includes gb:AA488672 /FEA=EST /DB_XREF=gi:2216103 /DB_XREF=est:ab40d10.s1 /CLONE=IMAGE:843283
204334_at	/UG=Hs.21599 Kruppel-like factor 7 (ubiquitous) /FL=gb:AB015132.1 gb:NM_003709.1
	Consensus includes gb:BF435809 /FEA=EST /DB_XREF=gi:11448124 /DB_XREF=est:nab42a09.x1 /CLONE=IMAGE:3268504
203531_at	/UG=Hs.101299 cullin 5 /FL=gb:AF327710.1 gb:AF017061.1 gb:NM_003478.1
	gb:NM_005197.1 /DEF=Homo sapiens checkpoint suppressor 1 (CHES1), mRNA. /FEA=mrna /GEN=CHES1 /PROD=checkpoint suppressor
205022_s_at	1 /DB_XREF=gi:4885136 /UG=Hs.211773 checkpoint suppressor 1 /FL=gb:U68723.1 gb:NM_005197.1
	gb:NM_002788.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3), mRNA. /FEA=mrna
201532_at	/GEN=PSMA3 /PROD=proteasome (prosome, macropain) subunit, alpha type, 3 /DB_XREF=gi:4506182 /UG=Hs.167106 proteasome (prosome, macropain) subunit, alpha type, 3 /FL=gb:BC005265.1 gb:NM_002788.1
	gb:NM_016817.1 /DEF=Homo sapiens 2-5oligoadenylate synthetase 2 (OAS2), transcript variant 1, mRNA. /FEA=mrna /GEN=OAS2
	/PROD=2-5oligoadenylate synthetase 2, isoform p71 /DB_XREF=gi:8051624 /UG=Hs.264981 2-5oligoadenylate synthetase 2
204972_at	/FL=gb:N87434.1 gb:NM_016817.1
	Consensus includes gb:AL536517 /FEA=EST /DB_XREF=gi:12800010 /DB_XREF=est:AL536517 /CLONE=CSODF038YH13 (5 prime)
	/UG=Hs.78995 MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) /FL=gb:L08895.1
209200_at	gb:NM_025238.1 /DEF=Homo sapiens BTB (POZ) domain containing 1 (BTBD1), mRNA. /FEA=mrna /GEN=BTBD1 /PROD=BTB (POZ) domain containing 1 /DB_XREF=gi:13376847 /UG=Hs.21332 BTB (POZ) domain containing 1 /FL=gb:AL136853.1
217945_at	gb:AF257241.1 gb:NM_025238.1 gb:AF355402.1
	gb:NM_012111.1 /DEF=Homo sapiens chromosome 14 open reading frame 3 (C14ORF3), mRNA. /FEA=mrna /GEN=C14ORF3
	/PROD=chromosome 14 open reading frame 3 /DB_XREF=gi:6912279 /UG=Hs.204041 chromosome 14 open reading frame 3
201491_at	/FL=gb:BC000321.1 gb:NM_012111.1 gb:AF164791.1
	gb:NM_001545.1 /DEF=Homo sapiens immature colon carcinoma transcript 1 (ICT1), mRNA. /FEA=mrna /GEN=ICT1
	/PROD=immature colon carcinoma transcript 1 /DB_XREF=gi:4557656 /UG=Hs.9078 immature colon carcinoma transcript 1
204868_at	/FL=gb:NM_001545.1
	gb:NM_016021.1 /DEF=Homo sapiens CGI-76 protein (LOC51632), mRNA. /FEA=mrna /GEN=LOC51632 /PROD=CGI-76 protein
217826_s_at	/DB_XREF=gi:7706311 /UG=Hs.184325 CGI-76 protein /FL=gb:AF151834.1 gb:AF151834.1 gb:AF151039.1 gb:NM_016021.1
	Consensus includes gb:AUI144066 /FEA=EST /DB_XREF=gi:11005587 /DB_XREF=est:AUI144066 /CLONE=HEMBA1000798
212534_at	/UG=Hs.285519 Homo sapiens cDNA FLJ11904 fis, clone HEMBB1000048
	gb:BC000324.1 /DEF=Homo sapiens, similar to granulin, clone MGC:8480, mRNA, complete cds. /FEA=mrna /PROD=Similar to
211284_s_at	granulin /DB_XREF=gi:12653114 /UG=Hs.180577 granulin /FL=gb:BC000324.1
	Consensus includes gb:AA551075 /FEA=EST /DB_XREF=gi:2321327 /DB_XREF=est:nk74h06.s1 /CLONE=IMAGE:1019291
212188_at	/UG=Hs.109438 Homo sapiens clone 24775 mRNA sequence



201458_s_at	gb:NM_004725.1 /DEF=Homo sapiens BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3), mRNA. /FEA=mRNA /GEN=BUB3 /PROD=BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /DB_XREF=gi:4757879 /UG=Hs.40323 BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /FL=gb:BC005138.1 gb:AF047472.1 gb:AF053304.1 gb:AF081496.1
201458_s_at	gb:NM_004725.1
201773_at	gb:NM_015339.1 /DEF=Homo sapiens activity-dependent neuroprotective protein (ADNP), mRNA. /FEA=mRNA /GEN=ADNP /PROD=activity-dependent neuroprotective protein /DB_XREF=gi:12229216 /UG=Hs.3657 activity-dependent neuroprotective protein /FL=gb:AF250860.1 gb:NM_015339.1
218751_s_at	gb:NM_018315.1 /DEF=Homo sapiens hypothetical protein FLJ11071 (FLJ11071), mRNA. /FEA=mRNA /GEN=FLJ11071 /PROD=hypothetical protein FLJ11071 /DB_XREF=gi:8922851 /UG=Hs.31945 hypothetical protein FLJ11071 /FL=gb:NM_018315.1
201350_at	gb:NM_004475.1 /DEF=Homo sapiens flotillin 2 (FLOT2), mRNA. /FEA=mRNA /GEN=FLOT2 /PROD=flotillin 2 /DB_XREF=gi:4758393 /UG=Hs.184488 flotillin 2 FL=gb:NM_004475.1 gb:MG0922.1
	gb:NM_004766.1 /DEF=Homo sapiens coatomer protein complex, subunit beta 2 (beta prime) (COPB2), mRNA. /FEA=mRNA /GEN=COPB2
201098_at	/PROD=coatomer protein complex, subunit beta 2 (betaprime) /DB_XREF=gi:4758031 /UG=Hs.75724 coatomer protein complex, subunit beta 2 (beta prime) /FL=gb:BC000326.1 gb:NM_004766.1
	gb:NM_016213.1 /DEF=Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), mRNA. /FEA=mRNA /GEN=TRIP4 /PROD=activating signal cointegrator 1 /DB_XREF=gi:7706430 /UG=Hs.116784 thyroid hormone receptor interactor 4 /FL=gb:AF168418.1 gb:NM_016213.1
203732_at	gb:NM_002642.1 /DEF=Homo sapiens phosphatidylinositol glycan, class C (PIGC), mRNA. /FEA=mRNA /GEN=PIGC /PROD=phosphatidylinositol glycan, class C /DB_XREF=gi:4505794 /UG=Hs.75790 phosphatidylinositol glycan, class C /FL=gb:D85418.1 gb:NM_002642.1
202846_s_at	gb:NM_002115.1 /DEF=Homo sapiens hexokinase 3 (white cell) (HK3), mRNA. /FEA=mRNA /GEN=HK3 /PROD=hexokinase 3 (white cell) /DB_XREF=gi:4504394 /UG=Hs.159237 hexokinase 3 (white cell) /FL=gb:U51333.1 gb:NM_002115.1
205936_s_at	gb:NM_004964.2 /DEF=Homo sapiens histone deacetylase 1 (HDAC1), mRNA. /FEA=mRNA /GEN=HDAC1 /PROD=histone deacetylase 1 /DB_XREF=gi:13128859 /UG=Hs.88556 histone deacetylase 1 /FL=gb:BC000301.1 gb:U50079.1 gb:NM_004964.2 gb:D50405.1
201209_at	Consensus includes gb:AI123426 /FEA=EST /DB_XREF=gi:3539192 /DB_XREF=est:qa49c09.x1 /CLONE=IMAGE:1690096 /UG=Hs.239720 CCR4-NOT transcription complex, subunit 2 /FL=gb:AF113226.1 gb:AF180473.1 gb:NM_014515.1
217798_at	Consensus includes gb:BE963245 /FEA=EST /DB_XREF=gi:11766663 /DB_XREF=est:601656874r1 /CLONE=IMAGE:3865699 /UG=Hs.21229 f-box and WD-40 domain protein 1B /FL=gb:AF176022.1 gb:AB033281.1
209455_at	Consensus includes gb:AL137751.1 /DEF=Homo sapiens mRNA; cDNA DKFp434I0812 (from clone DKFp434I0812); partial cds. /FEA=mRNA /GEN=DKFp434I0812 /PROD=hypothetical protein /DB_XREF=gi:6808387 /UG=Hs.263671 Homo sapiens mRNA; cDNA DKFp434I0812 (from clone DKFp434I0812); partial cds
212397_at	gb:NM_006117.1 /DEF=Homo sapiens peroxisomal D3, D2-enoyl-CoA isomerase (PECI), mRNA. /FEA=mRNA /GEN=PECI /PROD=peroxisomal D3, D2-enoyl-CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3, D2-enoyl-CoA isomerase /FL=gb:AL136642.1 gb:BC002668.1 gb:AF069301.1 gb:AF153612.1 gb:NM_006117.1 gb:AF244138.1
218025_s_at	gb:NM_003896.1 /DEF=Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), mRNA. /FEA=mRNA /GEN=SIAT9 /PROD=sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /DB_XREF=gi:4506954 /UG=Hs.225939 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /FL=gb:AB018356.1 gb:NM_003896.1 gb:AF119415.1
203217_s_at	Consensus includes gb:AI700633 /FEA=EST /DB_XREF=gi:4988533 /DB_XREF=est:we38g03.x1 /CLONE=IMAGE:2343412 /UG=Hs.288232
212812_at	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970
	gb:NM_002713.1 /DEF=Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 8 (PP1R8), mRNA. /FEA=mRNA /GEN=PP1R8 /PROD=protein phosphatase 1, regulatory (inhibitor) subunit 8 /DB_XREF=gi:4506014 /UG=Hs.78961 protein phosphatase 1, regulatory (inhibitor) subunit 8 /FL=gb:NM_002713.1 gb:U14575.1
207830_s_at	gb:NM_005044.1 /DEF=Homo sapiens protein kinase, X-linked (PRKX), mRNA. /FEA=mRNA /GEN=PRKX /PROD=protein kinase, X-linked /DB_XREF=gi:4826947 /UG=Hs.147996 protein kinase, X-linked /FL=gb:NM_005044.1

215633_x_at	Consensus includes gb:AV713720 /FEA=EST /DB_XREF=gi:10795237 /DB_XREF=est:AV713720 /CLONE=DCBBVA12 /UG=Hs.306434 Homo sapiens mRNA for LST-IN protein
208660_at	gb:BC000105.1 /DEF=Homo sapiens, Similar to CG14740 gene product, clone MGC:2503, mRNA, complete cds. /FEA=mrna /PROD=Similar to CG14740 gene product /DB_XREF=gi:12652712 /UG=Hs.239760 citrate synthase /FL=gb:BC000105.1 gb:AF047042.1 gb:NM_004077.1
218805_at	gb:NM_018384.1 /DEF=Homo sapiens hypothetical protein FLJ11296 (FLJ11296), mRNA. /FEA=mrna /GEN=FLJ11296 /PROD=hypothetical protein FLJ11296 /DB_XREF=gi:8922984 /UG=Hs.26194 hypothetical protein FLJ11296 /FL=gb:NM_018384.1 gb:NM_015640.1 /DEF=Homo sapiens PAI-1 mRNA-binding protein (PAI-RBP1), mRNA. /FEA=mrna /GEN=PAI-RBP1 /PROD=PAI-1 mRNA-binding protein /DB_XREF=gi:7661625 /UG=Hs.165998 PAI-1 mRNA-binding protein /FL=gb:AL080119.1 gb:NM_015640.1 gb:NM_006513.1 /DEF=Homo sapiens seryl-tRNA synthetase (SARS), mRNA. /FEA=mrna /GEN=SARS /PROD=seryl-tRNA synthetase /DB_XREF=gi:5730028 /UG=Hs.4888 seryl-tRNA synthetase /FL=gb:BC000716.1 gb:NM_006513.1 gb:D49914.1
200802_at	Consensus includes gb:AI633709 /FEA=EST /DB_XREF=gi:4685039 /DB_XREF=est:th71f03.x1 /CLONE=IMAGE:2124125 /UG=Hs.30174
212303_at	small nuclear RNA activating complex, polypeptide 5, 19kD
204640_s_at	gb:NM_003563.1 /DEF=Homo sapiens speckle-type POZ protein (SPOP), mRNA. /FEA=mrna /GEN=SPOP /PROD=speckle-type POZ protein /DB_XREF=gi:4507182 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC003385.1 gb:NM_003563.1 gb:NM_022735.1 /DEF=Homo sapiens golgi resident protein GCP60 (GCP60), mRNA. /FEA=mrna /GEN=GCP60 /PROD=golgi resident protein GCP60 /DB_XREF=gi:12232390 /UG=Hs.6831 golgi resident protein GCP60 /FL=gb:AB043587.1 gb:NM_022735.1 gb:M80436.1 /DEF=Human platelet activating factor receptor mRNA, complete cds. /FEA=mrna /GEN=PTAFR /PROD=platelet activating factor receptor /DB_XREF=gi:189537 /FL=gb:M80436.1
211661_x_at	gb:AF050641.1 /DEF=Homo sapiens NADH-ubiquinone oxidoreductase 39kDa subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. /FEA=mrna /PROD=NADH-ubiquinone oxidoreductase 39kDa subunit /DB_XREF=gi:5326822 /UG=Hs.75227 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9
208969_at	(39kD) /FL=gb:AF050641.1 gb:NM_005002.1
202227_s_at	gb:NM_006696.1 /DEF=Homo sapiens thyroid hormone receptor coactivating protein (SMAP), mRNA. /FEA=mrna /GEN=SMAP /PROD=thyroid hormone receptor coactivating protein /DB_XREF=gi:5730052 /UG=Hs.5464 thyroid hormone receptor coactivating protein /FL=gb:AF016270.1 gb:NM_006696.1
221989_at	Consensus includes gb:AW057781 /FEA=EST /DB_XREF=gi:5933420 /DB_XREF=est:wx03f09.x1 /CLONE=IMAGE:2542601 /UG=Hs.29797 ribosomal protein L10
202545_at	gb:NM_006254.1 /DEF=Homo sapiens protein kinase C, delta (PRKCD), mRNA. /FEA=mrna /GEN=PRKCD /PROD=protein kinase C, delta /DB_XREF=gi:5453969 /UG=Hs.155342 protein kinase C, delta /FL=gb:D07860.1 gb:D07861.1 gb:D10495.1 gb:NM_006254.1 gb:NM_003588.1 /DEF=Homo sapiens cullin 4B (CUL4B), mRNA. /FEA=mrna /GEN=CUL4B /PROD=cullin 4B /DB_XREF=gi:13270466 /UG=Hs.155976 cullin 4B /FL=gb:NM_003588.1 gb:AB014595.1
202214_s_at	gb:NM_022734.1 /DEF=Homo sapiens hypothetical protein FLJ20859 (FLJ20859), mRNA. /FEA=mrna /GEN=FLJ20859 /PROD=hypothetical protein FLJ20859 /DB_XREF=gi:12232388 /UG=Hs.6311 hypothetical protein FLJ20859 /FL=gb:NM_022734.1 gb:NM_017829.1 /DEF=Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA. /FEA=mrna /GEN=FLJ20454 /PROD=hypothetical protein FLJ20454 /DB_XREF=gi:8923424 /UG=Hs.26890 hypothetical protein FLJ20454 /FL=gb:AF273271.1 gb:NM_017829.1
218592_s_at	gb:AF164598.1 /DEF=Homo sapiens cell division control protein 16 (CDC16) mRNA, complete cds. /FEA=mrna /GEN=CDC16 /PROD=cell division control protein 16 /DB_XREF=gi:5533374 /UG=Hs.1592 CDC16 (cell division cycle 16, S. cerevisiae, homolog) /FL=gb:AF164598.1
209658_at	gb:NM_004649.1 /DEF=Homo sapiens ESI (zebrafish) protein, human homolog of (C21ORF33), mRNA. /FEA=mrna /GEN=C21ORF33 /PROD=ESI (zebrafish) protein, human homolog of /DB_XREF=gi:5031690 /UG=Hs.182423 ESI (zebrafish) protein, human homolog of /FL=gb:BC002370.1 gb:BC003587.1 gb:D86061.1 gb:U53003.1 gb:NM_004649.1
202217_at	Cluster Incl. AA868332:ak40405.sl Homo sapiens cDNA, 3 end /clone=IMAGE-1408473 /clone_end=3 /gb=AA868332 /gi=2963777 /ug=Hs.77978 /len=481
54970_at	

202441_at	Consensus includes gb:AL568449 /FEA=EST /DB_XREF=gi:12922799 /DB_XREF=est:AL568449 /CLONE=CS0DE001YC12 (3 prime) /UG=Hs.285818 similar to Caenorhabditis elegans protein C42C1.9 /FL=gb:AF064093.1 gb:NM_006459.1
211383_s_at	gb:AL136827.1 /DEF=Homo sapiens mRNA; cDNA DKFp434F2427 (from clone DKFp434F2427); complete cds. /FEA=mrna /GEN=DKFp434F2427 /PROD=hypothetical protein /DB_XREF=gi:6807664 /UG=Hs.27207 KIAA0982 protein /FL=gb:AL136827.1 /GEN=NM_003365.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase core protein I (UQCRC1), mRNA. /FEA=mrna /GEN=UQCRC1 /PROD=ubiquinol-cytochrome c reductase core protein I /DB_XREF=gi:4507840 /UG=Hs.119251 ubiquinol-cytochrome c reductase core protein I /FL=gb:L16842.1 gb:NM_003365.1 gb:D26485.1
201903_at	gb:AF113019.1 /DEF=Homo sapiens PRO2451 mRNA, complete cds. /FEA=mrna /PROD=PRO2451 /DB_XREF=gi:6642761 /UG=Hs.250581 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
201827_at	/FL=gb:U66618.1 gb:NM_003077.1 gb:AF113019.1
201583_s_at	gb:NM_006363.1 /DEF=Homo sapiens Sec23 (S. cerevisiae) homolog B (SEC23B), mRNA. /FEA=mrna /GEN=SEC23B /PROD=Sec23 (S. cerevisiae) homolog B /DB_XREF=gi:5454043 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /FL=gb:BC005404.1 gb:NM_006363.1
210825_s_at	gb:AF130103.1 /DEF=Homo sapiens clone FLB2914 PRO0720 mRNA, complete cds. /FEA=mrna /PROD=PRO0720 /DB_XREF=gi:11493509 /UG=Hs.160483 erythrocyte membrane protein band 7.2 (stomatatin) /FL=gb:AF130103.1
212696_s_at	Consensus includes gb:BF968633 /FEA=EST /DB_XREF=gi:12335848 /DB_XREF=est:602271068F1 /CLONE=IMAGE:4359209 /UG=Hs.66394 ring finger protein 4
218229_s_at	gb:NM_017542.1 /DEF=Homo sapiens KIAA1513 protein (KIAA1513), mRNA. /FEA=mrna /GEN=KIAA1513 /PROD=KIAA1513 protein /DB_XREF=gi:8923835 /UG=Hs.284227 KIAA1513 protein /FL=gb:NM_017542.1
210111_s_at	gb:AF277175.1 /DEF=Homo sapiens PNAS-138 mRNA, complete cds. /FEA=mrna /PROD=PNAS-138 /DB_XREF=gi:12751080 /UG=Hs.326790 Homo sapiens PNAS-138 mRNA, complete cds. /FL=gb:AF277175.1
201268_at	gb:NM_002512.1 /DEF=Homo sapiens non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=NME2 /PROD=non-metastatic cells 2, protein (NM23B) expressed in /DB_XREF=gi:4505408 /UG=Hs.275163 non-metastatic cells 2, protein (NM23B) expressed in /FL=gb:BC002476.1 gb:M36981.1 gb:L16785.1 gb:NM_002512.1
201199_s_at	gb:NM_002807.1 /DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), mRNA. /FEA=mrna /GEN=PSMD1 /PROD=proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /DB_XREF=gi:4506224 /UG=Hs.3887 proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /FL=gb:D44466.1 gb:NM_002807.1
218242_s_at	gb:NM_017635.1 /DEF=Homo sapiens hypothetical protein FLJ20039 (FLJ20039), mRNA. /FEA=mrna /GEN=FLJ20039 /PROD=hypothetical protein FLJ20039 /DB_XREF=gi:8923045 /UG=Hs.267448 hypothetical protein FLJ20039 /FL=gb:NM_017635.1
201232_s_at	gb:NM_002817.1 /DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (PSMD13), mRNA. /FEA=mrna /GEN=PSMD13 /PROD=proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 /DB_XREF=gi:4506222 /UG=Hs.275554 proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 /FL=gb:BC001100.1 gb:BC001747.1 gb:AB009398.1
220044_x_at	gb:NM_002817.1 gb:AF083245.1 gb:AF107837.1
210835_s_at	gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mRNA. /FEA=mrna /GEN=LUC7A /PROD=cisplatin resistance-associated overexpressed protein /DB_XREF=gi:7706534 /UG=Hs.3688 cisplatin resistance-associated overexpressed protein /FL=gb:NM_016424.1
211271_x_at	gb:AF222711.1 /DEF=Homo sapiens ribeye mRNA, complete cds. /FEA=mrna /PROD=ribeye /DB_XREF=gi:12034652 /UG=Hs.171391 C-terminal binding protein 2 /FL=gb:AF222711.1 gb:NM_022802.1
218998_at	gb:BC004383.1 /DEF=Homo sapiens, Similar to polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I), clone MGC:10830, mRNA, complete cds. /FEA=mrna /PROD=Similar to polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) /DB_XREF=gi:13325139 /UG=Hs.172550 polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) /FL=gb:BC004383.1
201765_s_at	gb:NM_017832.1 /DEF=Homo sapiens hypothetical protein FLJ20457 (FLJ20457), mRNA. /FEA=mrna /GEN=FLJ20457 /PROD=hypothetical protein FLJ20457 /DB_XREF=gi:8923430 /UG=Hs.29276 hypothetical protein FLJ20457 /FL=gb:AF153417.1 gb:NM_017832.1
	Consensus includes gb:AL523158 /FEA=EST /DB_XREF=gi:12786651 /DB_XREF=est:AL523158 /CLONE=CS0DC001YM06 (3 prime)

2204837_at	UG-Hs.119403 hexosaminidase A (alpha polypeptide) /FL-gb:NM_000520.2	
2201221_s_at	Consensus includes gb:AL080178.1 /DEF=Homo sapiens mRNA; cDNA DKFp434K171 (from clone DKFp434K171); partial cds. /FEA-mRNA /GEN=DKFp434K171 /PROD=hypothetical protein /DB_XREF=gi:5262652 /UG-Hs.27194 DKFp434K171 protein /FL-gb:NM_015458.1	
2209092_s_at	gb:NM_003089.1 /DEF=Homo sapiens small nuclear ribonucleoprotein 70kd polypeptide (RNP antigen) (SNRP70), mRNA. /FEA-mRNA /GEN=SNRP70 /PROD=small nuclear ribonucleoprotein 70kd polypeptide (RNP antigen) /DB_XREF=gi:4507118 /UG-Hs.174051 small nuclear ribonucleoprotein 70kd polypeptide (RNP antigen) /FL-gb:BC000342.1 gb:M22636.1 gb:NM_003089.1	
2202265_at	gb:AF061730.1 /DEF=Homo sapiens clone 016b03 MY027 protein mRNA, complete cds. /FEA-mRNA /PROD=MY027 protein /DB_XREF=gi:12001995 /UG-Hs.279061 CGI-150 protein /FL-gb:AF061730.1 gb:AF151908.1 gb:NM_016080.1	
2203721_s_at	gb:NM_005180.1 /DEF=Homo sapiens murine leukemia viral (bmi-1) oncogene homolog (bmi-1) oncogene homolog /FL-gb:U13689.1 gb:NM_005180.1 viral (bmi-1) oncogene homolog /DB_XREF=gi:4885094 /UG-Hs.431 murine leukemia viral (bmi-1) oncogene homolog /DB_XREF=gi:7705764	
2202475_at	gb:NM_016001.1 /DEF=Homo sapiens CGI-48 protein (LOC51096), mRNA. /FEA-mRNA /GEN=LOC51096 /PROD=CGI-48 protein /DB_XREF=gi:113543641 /UG-Hs.6153 CGI-48 protein /FL-gb:AF151806.1 gb:NM_016001.1	
221213198_at	gb:NM_006326.1 /DEF=Homo sapiens seven transmembrane domain protein (NIFIE14), mRNA. /FEA-mRNA /GEN=NIFIE14 /PROD=seven transmembrane domain protein /DB_XREF=gi:5453781 /UG-Hs.9234 seven transmembrane domain protein /FL-gb:BC001118.1 gb:NM_006326.1	
2212837_at	Consensus includes gb:AI041204 /FEA=EST /DB_XREF=gi:3280398 /DB_XREF=est:ov7/g06.xl /CLONE=IMAGE:1643386 /UG-Hs.323748 Homo sapiens clone CDBP0086 mRNA sequence	
2206592_s_at	Consensus includes gb:AL117643.1 /DEF=Homo sapiens mRNA; cDNA DKFp434M245 (from clone DKFp434M245) /FEA-mRNA /GEN=DKFp434M245 /PROD=adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA. /FEA-mRNA /GEN=AP3D1 /PROD=adaptor-related protein complex 3, delta 1 subunit	
2212694_s_at	Consensus includes gb:D63877.1 /DEF=Human mRNA for KIAA0157 gene, partial cds. /FEA-mRNA /GEN=KIAA0157 /PROD=unknown (protein for MGC:14625) /DB_XREF=gi:113543641 /FL-gb:BC005969.1	
2211759_x_at	Consensus includes gb:AL050205.1 /DEF=Homo sapiens mRNA; cDNA DKFp586F1323 (from clone DKFp586F1323). /FEA-mRNA /DB_XREF=gi:4884444 /UG-Hs.26613 Homo sapiens mRNA; cDNA DKFp586F1323 (from clone DKFp586F1323)	
2212714_at	Consensus includes gb:B0398414 /FEA=EST /DB_XREF=gi:13291862 /DB_XREF=est:602439888F1 /CLONE=IMAGE:4566380 /UG-Hs.84318 replication protein A1 (70kd) /FL-gb:M63488.1 gb:NM_002945.1	
2201528_at	gb:AF198052.1 /DEF=Homo sapiens EVH1 domain binding protein mRNA, complete cds. /FEA=CDS /PROD=EVH1 domain binding protein /DB_XREF=gi:7416992 /UG-Hs.58435 EVH1 domain binding protein (PXB-120130) /FL-gb:AF198052.1	
2211795_s_at	gb:NM_018394.1 /DEF=Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA. /FEA-mRNA /GEN=FLJ11342 /PROD=hypothetical protein FLJ11342	
2218633_x_at	gb:NM_018394.1 /DEF=Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA. /FEA-mRNA /GEN=FLJ11342 /PROD=hypothetical protein FLJ11342	
2208000_s_at	gb:NM_005345.3 /DEF=Homo sapiens heat shock 70kd protein 1A (HSPAL1), mRNA. /FEA-mRNA /GEN=HSPAL1 /PROD=heat shock 70kd protein 1A /DB_XREF=gi:5579469 /UG-Hs.8997 heat shock 70kd protein 1A /FL-gb:BC002453.1 gb:NM_005345.3	
2214719_at	Consensus includes gb:AK026720.1 /DEF=Homo sapiens cDNA: FLJ23067 fis, clone LNG04993	
2213655_at	Consensus includes gb:AA502643 /FEA=EST /DB_XREF=gi:2237610 /DB_XREF=est:ne42g05.sl /CLONE=IMAGE:900056 /UG-Hs.79474 tyrosine 3-monooxygenase activation protein, epsilon polypeptide	
2212371_at	Consensus includes gb:AL049397.1 /DEF=Homo sapiens mRNA; cDNA DKFp586C1019 (from clone DKFp586C1019); /FEA-mRNA /DB_XREF=gi:4500188 /UG-Hs.12314	
2210166_at	Homo sapiens mRNA; cDNA DKFp586C1019 (from clone DKFp586C1019)	
2217958_at	gb:AF051151.1 /DEF=Homo sapiens Tollinterleukin-1 receptor-like protein 3 (TIL3) mRNA, complete cds. /FEA-mRNA /GEN=TIL3 /PROD=Tollinterleukin-1 receptor-like protein 3 /DB_XREF=gi:3132525 /UG-Hs.114408 toll-like receptor 5 /FL-gb:AF051151.1	
	gb:NM_016146.1 /DEF=Homo sapiens PTD009 protein (PTD009), mRNA. /FEA-mRNA /GEN=PTD009 /PROD=PTD009 protein /DB_XREF=gi:7706666	

	UG=Hs.279901.PTD009 protein / FL=gb:AF151862.1 gb:AF161520.1 gb:NM_016146.1 gb:NM_024567.1 /DEF=Homo sapiens hypothetical protein FLJ21616 (FLJ21616), mRNA. /FEA=mrna /GEN=FLJ21616 /PROD=hypothetical protein FLJ21616 /DB_XREF=gi:13375737 /UG=Hs.14562 hypothetical protein FLJ21616 /FL=gb:NM_024567.1
219269_at	gb:NM_017923.1 /DEF=Homo sapiens hypothetical protein FLJ20668 (FLJ20668), mRNA. /FEA=mrna /GEN=FLJ20668 /PROD=hypothetical protein FLJ20668 /DB_XREF=gi:8923612 /UG=Hs.12920 hypothetical protein FLJ20668 /FL=gb:NM_017923.1
219574_at	gb:AF112222.1 /DEF=Homo sapiens nuclear protein SDK3 mRNA, complete cds. /FEA=mrna /PROD=nuclear protein SDK3 /DB_XREF=gi:5563229 /UG=Hs.44499 pinin, desmosome associated protein /FL=gb:AF112222.1
210183_x_at	gb:AF000424.1 /DEF=Homo sapiens LST1 mRNA, complete cds. /FEA=mrna /GEN=LST1 /DB_XREF=gi:2145063 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:AF000424.1
211582_x_at	Consensus includes gb:AB011148.1 /DEF=Homo sapiens mRNA for KIAA0576 protein, partial cds. /FEA=mrna /GEN=KIAA0576 /PROD=KIAA0576 protein / DB_XREF=gi:3043675 /UG=Hs.172329 KIAA0576 protein
212557_at	Consensus includes gb:AB033066.1 /DEF=Homo sapiens mRNA for KIAA1240 protein, partial cds. /FEA=mrna /GEN=KIAA1240 /PROD=KIAA1240 protein / DB_XREF=gi:6330790 /UG=Hs.62576 KIAA1240 protein
213387_at	gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mrna /GEN=SCAMP2 /PROD=secretory carrier membra- ne protein 2 /DB_XREF=gi:5730030 /UG=Hs.238030 secretory carrier membrane protein 2 /FL=gb:BC001376.1 gb:BC004385.1 gb:AF005038.2 gb:NM_005697.2
218143_s_at	gb:M92439.1 /DEF=Human leucine-rich protein mRNA, complete cds. /FEA=mrna /PROD=leucine-rich protein; leucine-rich protein /DB_XREF=gi:177109 /FL=gb:M92439.1
211615_s_at	Consensus includes gb:W74620 /FEA=EST /DB_XREF=gi:1384833 /DB_XREF=est:zd77e04.s1 /CLONE=IMAGE:34686 /UG=Hs.303627 heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD)
213359_at	gb:NM_016019.1 /DEF=Homo sapiens CGI-74 protein (LOC51631), mRNA. /FEA=mrna /GEN=LOC51631 /PROD=CGI-74 protein /DB_XREF=gi:7706309 /UG=Hs.7194 CGI-74 protein /FL=gb:AF151832.1 gb:NM_016019.1
217842_at	gb:NM_015416.1 /DEF=Homo sapiens DKFZF586A011 protein (DKFZF586A011), mRNA. /FEA=mrna /GEN=DKFZF586A011 /PROD=DKFZF586A011 protein /DB_XREF=gi:7661659 /UG=Hs.75884 DKFZF586A011 protein /FL=gb:NM_015416.1
207170_s_at	Consensus includes gb:BF673699 /FEA=EST /DB_XREF=gi:1947594 /DB_XREF=est:602136277 /CLONE=IMAGE:4272774 /UG=Hs.184050 v-Ki-ras2 Kirsten- rat sarcoma 2 viral oncogene homolog
214352_s_at	gb:NM_012199.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA. /FEA=mrna /GEN=EIF2C1 /PROD=eukaryotic translation initiation factor 2C, 1 /DB_XREF=gi:6912351 /UG=Hs.14520 eukaryotic translation initiation factor 2C, 1 /FL=gb:AF093097.1 gb:NM_012199.1
218287_s_at	gb:NM_001803.1 /DEF=Homo sapiens CDW52 antigen (CAMPATH-1 antigen) (CDW52), mRNA. /FEA=mrna /GEN=CDW52 /PROD=CDW52 antigen (CAMPATH-1 anti- gen) /DB_XREF=gi:4502760 /UG=Hs.276770 CDW52 antigen (CAMPATH-1 antigen) /FL=gb:BC000644.1 gb:NM_001803.1
204661_at	gb:NM_014280.1 /DEF=Homo sapiens splicing factor similar to dnal (SPF31), mRNA. /FEA=mrna /GEN=SPF31 /PROD=splicing factor similar to dnal /DB_XREF=gi:7657610 /UG=Hs.74711 Dnal (Hsp40) homolog, subfamily C, member 8 /FL=gb:AF083190.1 gb:NM_014280.1
205545_x_at	Consensus includes gb:AA928506 /FEA=EST /DB_XREF=gi:3076797 /DB_XREF=est:oml7g03.s1 /CLONE=IMAGE:1541332 /UG=Hs.10762 ESTS Consensus includes gb:AU158148 /FEA=EST /DB_XREF=gi:11019669 /DB_XREF=est:AU158148 /CLONE=FLAC1011221 /UG=Hs.321105 Homo sapiens cDNA: FLJ21737 fis, clone COLP3396
213750_at	gb:NM_018103.1 /DEF=Homo sapiens hypothetical protein FLJ10470 (FLJ10470), mRNA. /FEA=mrna /GEN=FLJ10470 /PROD=hypothetical protein FLJ10470 /DB_XREF=gi:8922441 /UG=Hs.44672 hypothetical protein FLJ10470 /FL=gb:NM_018103.1
219970_s_at	gb:M61715.1 /DEF=Human cryptophanyl-tRNA synthetase (WRS) mRNA, complete cds. /FEA=mrna /GEN=WARS /PROD=transfer RNA-Trip synthetase FLJ10470 /DB_XREF=gi:340367 /UG=Hs.82030 tryptophanyl-tRNA synthetase /FL=gb:M77804.1 gb:M61715.1 gb:NM_004184.2
218684_at	gb:NM_002582.1 /DEF=Homo sapiens poly(A)-specific ribonuclease (deadenylation nuclease) (PARN), mRNA. /FEA=mrna /GEN=PARN /PROD=poly(A)- specific ribonuclease (deadenylation nuclease) /DB_XREF=gi:4505610 /UG=Hs.43445 poly(A)-specific ribonuclease (deadenylation nuclease) /FL=gb:NM_002582.1
200628_s_at	Consensus includes gb:AA928506 /FEA=EST /DB_XREF=gi:3076797 /DB_XREF=est:oml7g03.s1 /CLONE=IMAGE:1541332 /UG=Hs.10762 ESTS Consensus includes gb:AU158148 /FEA=EST /DB_XREF=gi:11019669 /DB_XREF=est:AU158148 /CLONE=FLAC1011221 /UG=Hs.321105 Homo sapiens cDNA: FLJ21737 fis, clone COLP3396
203905_at	gb:NM_004364.1 /DEF=Homo sapiens CCNAenhancer binding protein (CEBP), alpha (CEBPA), mRNA. /FEA=mrna /GEN=CEBPA /PROD=CCNAenhancer bind- ing protein (CEBP), alpha /DB_XREF=gi:4757971 /UG=Hs.76171 CCNAenhancer binding protein (CEBP), alpha /FL=gb:NM_004364.1
204039_at	Cluster Incl. A1188402:q08e03.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1723132 /clone_end=3 /gb=A1188402 /gi=3739611 /ug=Hs.93391 /len=506
63009_at	gb:AY028632.1 /DEF=Homo sapiens catalase (CAT) mRNA, complete cds. /FEA=cds /GEN=CAT /PROD=catalase /DB_XREF=gi:13562131 /FL=gb:AY028632.1
211922_s_at	Consensus includes gb:BF690150 /FEA=EST /DB_XREF=gi:11975558 /DB_XREF=est:602186478T1 /CLONE=IMAGE:4298635 /UG=Hs.19210 ESTs
212861_at	

206715_at	gb:NM_012252.1 / DEF=Homo sapiens transcription factor EC (TFEC), mRNA. / FEA=mrna / GEN=TFEC / PROD=transcription factor EC / DB_XREF=gi:6912701 / UG=Hs.113274 transcription factor EC / FL=gb:AB014580.1 gb:NM_012252.1
213123_at	Consensus includes gb:BE222709 / FEA=EST / DB_XREF=gi:8910027 / DB_XREF=est:hu5106.x1 / CLONE=IMAGE:3173626 / UG=Hs.28785 microfibrillar-associated protein 3
204049_s_at	gb:NM_014721.1 / DEF=Homo sapiens KIAA0680 gene product (KIAA0680), mRNA. / FEA=mrna / GEN=KIAA0680 / PROD=KIAA0680 gene product
201985_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
208773_s_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
219563_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
218501_at	gb:NM_019555.1 / DEF=Homo sapiens KIAA0680 gene product (KIAA0680), mRNA. / FEA=mrna / GEN=KIAA0680 / PROD=KIAA0680 gene product
212833_at	Consensus includes gb:AW439494 / FEA=EST / DB_XREF=gi:6974800 / DB_XREF=est:xt19c01.x1 / CLONE=IMAGE:2779584 / UG=Hs.167531 methylcrotonoyl-Coenzyme A carboxylase 2 (beta) / FL=gb:AB050049.1 gb:AF310971.1 gb:AF301000.1 gb:NM_022132.2
209623_at	gb:BC002704.1 / DEF=Homo sapiens, Similar to signal transducer and activator of transcription 1, 91kd, clone MGC:3493, mRNA complete cds. / FEA=mrna / PROD=Similar to signal transducer and activator of transcription 1, 91kd / DB_XREF=gi:12803734 / UG=Hs.21486 signal transducer and activator of transcription 1, 91kd / FL=gb:BC002704.1
209969_s_at	gb:NM_017869.1 / DEF=Homo sapiens BANP homolog, SMAR1 homolog (FLJ20538), mRNA. / FEA=mrna / GEN=FLJ20538 / PROD=BANP homolog, SMAR1 homolog / DB_XREF=gi:8923506 / UG=Hs.194637 BANP homolog, SMAR1 homolog / FL=gb:NM_017869.1
219966_x_at	Consensus includes gb:W47179 / FEA=EST / DB_XREF=gi:1332046 / DB_XREF=est:zc34d07.s1 / CLONE=IMAGE:1324205 / UG=Hs.297939 cathepsin B
213275_x_at	gb:D45198.1 / DEF=Homo sapiens mRNA for template activating factor-1 alpha, complete cds. / FEA=mrna / GEN=set / PROD=template activating factor-1 alpha / DB_XREF=gi:971271 / UG=Hs.145279 SET translocation (myeloid leukemia-associated) / FL=gb:D45198.1
210231_x_at	Consensus includes gb:D87682.1 / DEF=Human mRNA for KIAA0241 gene, partial cds. / FEA=mrna / GEN=KIAA0241 / DB_XREF=gi:1663699 / UG=Hs.150275
212474_at	KIAA0241 protein
208717_at	gb:BC001669.1 gb:NM_005015.1
217527_s_at	Consensus includes gb:AI478300 / FEA=EST / DB_XREF=gi:4371526 / DB_XREF=est:tm39e01.x1 / CLONE=IMAGE:2160504 / UG=Hs.192789 ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H sapiens
220495_s_at	gb:NM_024745.1 / DEF=Homo sapiens hypothetical protein FLJ22625 (FLJ22625), mRNA. / FEA=mrna / GEN=FLJ22625 / PROD=hypothetical protein FLJ22625
200892_s_at	gb:NM_013451.1 / DEF=Homo sapiens fer-1 (C.elegans)-like 3 (myoferlin) / FL=gb:AF182316.1 gb:NM_013451.1
201798_s_at	gb:NM_002766.1 / DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA. / FEA=mrna / GEN=PRPSAP1 / PROD=phosphoribosyl pyrophosphate synthetase-associated protein 1
202529_at	gb:BC003360.1 / DEF=Homo sapiens, DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated) / DB_XREF=gi:13097182 / UG=Hs.100555 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Homo-regulated) / FL=gb:BC001238.1 gb:BC003360.1
208897_s_at	gb:BC005375.1 / DEF=Homo sapiens, peroxisomal membrane protein 3 (35kd, Zellweger syndrome) / DB_XREF=gi:13529226 / UG=Hs.180612 peroxisomal membrane protein 3 (35kd, Zellweger syndrome) / FL=gb:BC005375.1
210296_s_at	Consensus includes gb:BE738425 / FEA=EST / DB_XREF=gi:10152417 / DB_XREF=est:601572441T1 / CLONE=IMAGE:3833147 / UG=Hs.241507 ribosomal protein
212460_at	56



211800_s_at	gb:AF017306.1 /DEF=Homo sapiens deubiquitinating enzyme UnpES (UNP) mRNA, complete cds. /FEA=CDS /GEN=UNP /PROD=UnpES /DB_XREF=gi:2656142 /UG=Hs.77500 ubiquitin specific protease 4 (proto-oncogene) /FL=gb:AF017306.1
211800_s_at	gb:NM_002858.2 /DEF=Homo sapiens ATP-binding cassette, sub-family D (ALD), member 3 (ABCD3), mRNA. /FEA=mrna /GEN=ABCD3 /PROD=ATP-binding cassette, sub-family D, member 3 /DB_XREF=gi:10947125 /UG=Hs.76781 ATP-binding cassette, sub-family D (ALD), member 3 /FL=gb:NM_002858.2
202850_at	gb:M81182.1 /DEF=Homo sapiens ATP-binding cassette, sub-family D (ALD), member 3 (ABCD3), mRNA. /FEA=mrna /GEN=ABCD3 /PROD=ATP-binding cassette, sub-family D, member 3 /DB_XREF=gi:10947125 /UG=Hs.76781 ATP-binding cassette, sub-family D (ALD), member 3 /FL=gb:NM_002858.2
212202_s_at	Consensus includes gb:BG493972 /FEA=EST /DB_XREF=gi:13455486 /DB_XREF=est:602542222F1 /CLONE=IMAGE:4673316 /UG=Hs.16492 DZF2P564G2022 protein
209337_at	gb:AF063020.1 /DEF=Homo sapiens lens epithelium-derived growth factor mRNA, complete cds. /FEA=mrna /PROD=lens epithelium-derived growth factor /DB_XREF=gi:3283351 /UG=Hs.82110 PC4 and SFRS1 interacting protein 1 /FL=gb:NM_021144.1 gb:AF063020.1
207616_s_at	gb:NM_004180.1 /DEF=Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA. /FEA=mrna /GEN=TANK /PROD=TRAF family member-associated NFKB activator /DB_XREF=gi:4759249 /UG=Hs.146847 TRAF family member-associated NFKB activator /FL=gb:U63830.1 gb:NM_004180.1
204630_s_at	gb:NM_004871.1 /DEF=Homo sapiens golgi SNAP receptor complex member 1 (GOSR1), mRNA. /FEA=mrna /GEN=GOSR1 /PROD=golgi SNAP receptor complex member 1 /DB_XREF=gi:4758455 /UG=Hs.8868 golgi SNAP receptor complex member 1 /FL=gb:AF073926.1 gb:NM_004871.1
209422_at	Consensus includes gb:AL109965 /DEF=Human DNA sequence from clone RP5-1121G12 on chromosome 20 Contains the 3' end of a gene encoding two isoforms (the hepatocellular carcinoma-associated antigen 58 (HCA58) and a putative novel protein containing a PHD finger domain), the SCAND1 gene... /FEA=mrna.2 /DB_XREF=gi:9663113 /UG=Hs.112594 hypothetical protein DKFp434F0272 /FL=gb:AY027523.1 gb:AF348207.1
203658_at	gb:BC001689.1 /DEF=Homo sapiens, carnitineacylcarnitine translocase, clone MGC:1207, mRNA, complete cds. /FEA=mrna /PROD=carnitineacylcarnitine translocase /DB_XREF=gi:12804552 /UG=Hs.13845 solute carrier family 25 (carnitineacylcarnitine translocase), member 20 /FL=gb:BC001689.1 gb:NM_000387.2
212015_x_at	Consensus includes gb:RF690062 /FEA=EST /DB_XREF=gi:11975470 /DB_XREF=est:602186366T1 /CLONE=IMAGE:4298440 /UG=Hs.17550 polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I)
222122_s_at	Consensus includes gb:BG403671 /FEA=EST /DB_XREF=gi:13297119 /DB_XREF=est:602419393F1 /CLONE=IMAGE:4526326 /UG=Hs.16411 hypothetical protein LOC57187
202171_at	Consensus includes gb:AUI46275 /FEA=EST /DB_XREF=gi:11007796 /DB_XREF=est:AUI46275 /CLONE=HEMBB1000004 /UG=Hs.6557 zinc finger protein 161 /FL=gb:D28118.1 gb:NM_007146.1
210460_s_at	gb:AB033605.1 /DEF=Homo sapiens mRNA for PUB-R5, complete cds. /FEA=mrna /GEN=hpUB-R5 /PROD=hpUB-R5 /DB_XREF=gi:8918352 /UG=Hs.148495 proteasome (prosome, macropain) 26S subunit, non-APase, 4 /FL=gb:AB033605.1
207551_s_at	gb:NM_006800.1 /DEF=Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA. /FEA=mrna /GEN=MSL3L1 /PROD=male-specific lethal-3 (Drosophila)-like 1 /DB_XREF=gi:5803103 /UG=Hs.88764 male-specific lethal-3 (Drosophila)-like 1 /FL=gb:AF117065.1 gb:NM_006800.1
201104_x_at	gb:NM_015383.1 /DEF=Homo sapiens hypothetical protein (DU328E19.C1.1), mRNA. /FEA=mrna /GEN=DU328E19.C1.1 /PROD=hypothetical protein /DB_XREF=gi:7657016 /UG=Hs.218329 hypothetical protein /FL=gb:NM_015383.1
200812_at	gb:NM_006429.1 /DEF=Homo sapiens chaperonin containing TCP1, subunit 7 (eta) (CCT7), mRNA. /FEA=mrna /GEN=CCT7 /PROD=chaperonin containing TCP1, subunit 7 (eta) /DB_XREF=gi:5453606 /UG=Hs.108809 chaperonin containing TCP1, subunit 7 (eta) /FL=gb:AF026292.1 gb:NM_006429.1
203494_s_at	gb:NM_014679.1 /DEF=Homo sapiens KIAA0092 gene product /FL=gb:D42054.1 gb:NM_014679.1
202127_at	Consensus includes gb:AB011108.1 /DEF=Homo sapiens mRNA for KIAA0536 protein, partial cds. /FEA=mrna /GEN=KIAA0536 /PROD=KIAA0536 protein /DB_XREF=gi:3043595 /UG=Hs.198891 sexinethionein-protein kinase PRP4 homolog /FL=gb:U48736.1 gb:NM_003913.1
212532_s_at	Consensus includes gb:AW873564 /FEA=EST /DB_XREF=gi:8007617 /DB_XREF=est:h062c10.x1 /CLONE=IMAGE:3041970 /UG=Hs.155485 huntingtin interacting protein 2
218357_s_at	gb:NM_012459.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 8 (yeast) homolog B (TIMM8B), mRNA. /FEA=mrna /GEN=TIMM8B /PROD=translocase of inner mitochondrial membrane 8 (yeast) homolog B /DB_XREF=gi:6912711 /UG=Hs.279915 translocase of inner mitochondrial membrane 8
208847_s_at	gb:M29872.1 /DEF=Human alcohol dehydrogenase class III (ADH5) mRNA, complete cds. /FEA=mrna /GEN=ADH5 /DB_XREF=gi:178131 /UG=Hs.78989 alcohol dehydrogenase 5 (class III), chi polypeptide /FL=gb:NM_000671.2 gb:M29872.1 gb:M30471.1
207730_x_at	gb:NM_017932.1 /DEF=Homo sapiens hypothetical protein FLJ20700 (FLJ20700), mRNA. /FEA=mrna /GEN=FLJ20700 /PROD=hypothetical protein FLJ20700 /DB_XREF=gi:8923629 /UG=Hs.272222 hypothetical protein FLJ20700 /FL=gb:NM_017932.1
212896_at	Consensus includes gb:D29641.2 /DEF=Homo sapiens mRNA for KIAA0052 protein, partial cds. /FEA=mrna /GEN=KIAA0052 /PROD=KIAA0052 protein /DB_XREF=gi:6633994 /UG=Hs.278608 KIAA0052 protein
203156_at	gb:NM_016248.1 /DEF=Homo sapiens A-kinase anchoring protein 220 (LOCS1707), mRNA. /FEA=mrna /GEN=LOC51707 /PROD=A-kinase anchoring protein 220 /DB_XREF=gi:7706456 /UG=Hs.232076 A kinase (PRKA) anchor protein 11 /FL=gb:AF176555.1 gb:NM_016248.1
220066_at	gb:NM_022162.1 /DEF=Homo sapiens NOD2 protein (NOD2), mRNA. /FEA=mrna /GEN=NOD2 /PROD=NOD2 protein /DB_XREF=gi:11545911 /UG=Hs.135201 NOD2

[illegible]



209971_x.at	Consensus includes gb:A1928526 /FEA=EST /DB_XREF=gi:5664490 /DB_XREF=est:wp59a06.x1 /CLONE=IMAGE:2466034 /UG=Hs.258730 heme-regulated initiation factor 2-alpha kinase /FL=gb:AF116615.1
48580_at	Cluster Incl. U55777:HSU55777 Homo sapiens cDNA /clone=37698 /gb=U55777 /gi=1354513 /ug=Hs.180933 /len=1593 gb:NM_003315.1 /DEF=Homo sapiens tetratricopeptide repeat domain 2 (TTC2), mRNA. /FEA=mrna /GEN=TTCC2 /PROD=tetratricopeptide repeat domain 2 /DB_XREF=gi:4507712 /UG=Hs.5542 DnaJ (Hsp40) homolog, subfamily C, member 7 /FL=gb:U46571.1 gb:NM_003315.1
202416_at	gb:BC005895.1 /DEF=Homo sapiens, COX11 (yeast) homolog, cytochrome c oxidase assembly protein, clone MGC:14469, mRNA, complete cds. /FEA=mrna /PROD=COX11 (yeast) homolog, cytochrome c oxidase assembly protein /DB_XREF=gi:13543474 /FL=gb:BC005895.1
211727_s.at	gb:NM_015049.1 /DEF=Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA. /FEA=mrna /GEN=ALS2CR3 /PROD=amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 /DB_XREF=gi:13027379 /UG=Hs.154248 amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 /FL=gb:AB038951.1 gb:NM_015049.1
202125_s.at	gb:U59863.1 /DEF=Human TRAF-interacting protein 1-TRAF mRNA, complete cds. /FEA=mrna /PROD=I-TRAF /DB_XREF=gi:1518017 /UG=Hs.146847 TRAF family member-associated NFKB activator /FL=gb:U59863.1
209451_at	gb:BC001605.1 /DEF=Homo sapiens, phosphoribosyl pyrophosphate synthetase 1 /DB_XREF=gi:12804406 /UG=Hs.56 phosphoribosyl pyrophosphate synthetase 1 /FEA=mrna /PROD=phosphoribosyl pyrophosphate synthetase 1
209440_at	gb:NM_018946.2 /DEF=Homo sapiens N-acetylneuraminic acid phosphate synthase; sialic acid synthase (SAS), mRNA. /FEA=mrna /GEN=SAS /PROD=N-acetylneuraminic acid phosphate synthase; sialic acid synthase /FL=gb:NM_018946.2 gb:BC000008.1 gb:AF257466.1
218189_s.at	gb:NM_005271.1 /DEF=Homo sapiens glutamate dehydrogenase 1 (GLUD1), mRNA. /FEA=mrna /GEN=GLUD1 /PROD=glutamate dehydrogenase 1 /FL=gb:J03248.1 gb:M37154.1 gb:M20867.1 gb:NM_005271.1
200947_s.at	gb:NM_006323.1 /DEF=Homo sapiens SEC24 (S. cerevisiae) related gene family, member B (SEC24B), mRNA. /FEA=mrna /GEN=SEC24B /PROD=SEC24 (S. cerevisiae) related gene family, member B /DB_XREF=gi:5454045 /UG=Hs.7239 SEC24 (S. cerevisiae) related gene family, member B /FL=gb:NM_006323.1
202798_at	gb:NM_005955.1 /DEF=Homo sapiens metal-regulatory transcription factor 1 (MTF1), mRNA. /FEA=mrna /GEN=MTF1 /PROD=metal-regulatory transcription factor 1 /DB_XREF=gi:5174588 /UG=Hs.211581 metal-regulatory transcription factor 1 /FL=gb:NM_005955.1
205323_s.at	Consensus includes gb:N64760 /FEA=EST /DB_XREF=gi:1212589 /DB_XREF=est:y230c06.s1 /CLONE=IMAGE:284554 /UG=Hs.174905 KIAA0033 protein
212622_at	Consensus includes gb:BF055107 /FEA=EST /DB_XREF=gi:10809003 /DB_XREF=est:7175a05.x1 /CLONE=IMAGE:3392240 /UG=Hs.180789 S164 protein
212033_at	gb:NM_024699.1 /DEF=Homo sapiens hypothetical protein FLJ14007 (FLJ14007), mRNA. /FEA=mrna /GEN=FLJ14007 /PROD=hypothetical protein FLJ14007 /DB_XREF=gi:13375984 /UG=Hs.99519 hypothetical protein FLJ14007 /FL=gb:NM_024699.1
218919_at	gb:AB032251.1 /DEF=Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds. /FEA=mrna /GEN=BPTF /PROD=bromodomain PHD finger transcription factor /DB_XREF=gi:6683491 /UG=Hs.99872 fetal Alzheimer antigen /FL=gb:AB032251.1
209271_at	Consensus includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5
213322_at	Consensus includes gb:AW469184 /FEA=EST /DB_XREF=gi:7039290 /DB_XREF=est:hc78g04.x1 /CLONE=IMAGE:2898870 /UG=Hs.65406 ESTs
221895_at	Consensus includes gb:AAL76780 /FEA=EST /DB_XREF=gi:1757929 /DB_XREF=est:zp32a10.s1 /CLONE=IMAGE:611130 /UG=Hs.14512 D1PB protein /FL=gb:NM_017583.1
217760_at	Consensus includes gb:AL046419 /FEA=EST /DB_XREF=gi:5434493 /DB_XREF=est:DKFp434N247.s1 /CLONE=DKFp434N247 /UG=Hs.239489 TIAL cytotoxic granule-associated RNA-binding protein /FL=gb:NM_022037.1 gb:M77142.1
201448_at	gb:NM_018126.1 /DEF=Homo sapiens hypothetical protein FLJ10525 (FLJ10525), mRNA. /FEA=mrna /GEN=FLJ10525 /PROD=hypothetical protein FLJ10525 /DB_XREF=gi:8922490 /UG=Hs.31082 hypothetical protein FLJ10525 (FLJ10525), mRNA. /FEA=mrna /GEN=FLJ10525
218465_at	Consensus includes gb:AB011131 /DEF=Homo sapiens mRNA for KIAA0541 protein, partial cds. /FEA=mrna /GEN=KIAA0541 protein /DB_XREF=gi:3043605 /UG=Hs.10881 WD repeat domain 7
212880_at	gb:NM_016302.1 /DEF=Homo sapiens protein x 0001 (LOC51185), mRNA. /FEA=mrna /GEN=LOC51185 /PROD=protein x 0001 /DB_XREF=gi:10047097 /UG=Hs.18925 protein x 0001 /FL=gb:NM_016302.1 gb:AF117230.1
218142_s.at	gb:NM_003653.1 /DEF=Homo sapiens COP9 (constitutive photomorphogenic, Arabidopsis), subunit 3 (COP9), mRNA. /FEA=mrna /GEN=COP9 /PROD=COP9 (constitutive photomorphogenic, Arabidopsis), subunit 3 /DB_XREF=gi:4502974 /UG=Hs.6076 COP9 (constitutive photomorphogenic, Arabidopsis), subunit 3
202078_at	

	genic, Arabidopsis, homolog) subunit 3 /FL=gb:BC001891.1 gb:AF031647.1 gb:NM_003653.1 gb:AF098109.1	
219069_at	gb:NM_017704.1 /DEF=Homo sapiens hypothetical protein FLJ20189 (FLJ20189), mRNA. /FEA=mrna /GEN=FLJ20189 /PROD=hypothetical protein FLJ20189 /DB_XREF=gi:8923180 /UG=Hs.29052 hypothetical protein FLJ20189 /FL=gb:NM_017704.1	
218333_at	gb:NM_016041.1 /DEF=Homo sapiens CGI-101 protein (LOC51009), mRNA. /FEA=mrna /GEN=LOC51009 /PROD=CGI-101 protein /DB_XREF=gi:7705603 /UG=Hs.286131 CGI-101 protein /FL=gb:AF132289.1 gb:AF151859.1 gb:NM_016041.1 gb:AF242523.1	
213082_s_at	Consensus includes gb:AJ005866.1 /DEF=Homo sapiens mRNA for putative Sqv-7-like protein, partial. /FEA=mrna /PROD=Sqv-7-like protein /DB_XREF=gi:4008516 /UG=Hs.90078 nucleotide-sugar transporter similar to C. elegans sqv-7	
221452_s_at	gb:NM_030969.1 /DEF=Homo sapiens hypothetical protein MGC1223 (MGC1223), mRNA. /FEA=CDS /GEN=MGC1223 /PROD=hypothetical protein MGC1223 /DB_XREF=gi:13624338 /FL=gb:NM_030969.1	
213733_at	Consensus includes gb:BF740152 /FEA=EST /DB_XREF=gi:12066828 /DB_XREF=est:7n13g08.x1 /CLONE=IMAGE:3564495 /UG=Hs.121555 myosin IE	
201225_s_at	gb:NM_005839.1 /DEF=Homo sapiens SerArg-related nuclear matrix protein (plenty of prolines 101-like) (SRM160), mRNA. /FEA=mrna /GEN=SRM160 /PROD=SerArg-related nuclear matrix protein (plenty of prolines 101-like) /DB_XREF=gi:5032118 /UG=Hs.18192 SerArg-related nuclear matrix protein (plenty of prolines 101-like) /FL=gb:AF048977.1 gb:NM_005839.1	
219392_x_at	gb:NM_018304.1 /DEF=Homo sapiens hypothetical protein FLJ11029 (FLJ11029), mRNA. /FEA=mrna /GEN=FLJ11029 /PROD=hypothetical protein FLJ11029 /DB_XREF=gi:8922831 /UG=Hs.27448 hypothetical protein FLJ11029 /FL=gb:NM_018304.1	
219212_at	gb:NM_016299.1 /DEF=Homo sapiens heat shock protein hsp70-related protein (LOC51182), mRNA. /FEA=mrna /GEN=LOC51182 /PROD=heat shock protein hsp70-related protein /DB_XREF=gi:10047093 /UG=Hs.44581 heat shock protein hsp70-related protein /FL=gb:NM_016299.1 gb:AF112210.1	
217907_at	gb:AF143723.1	
200727_s_at	gb:NM_014161.1 /DEF=Homo sapiens HSPC071 protein (HSPC071), mRNA. /FEA=mrna /GEN=HSPC071 /PROD=HSPC071 protein /DB_XREF=gi:7661777 /UG=Hs.23038 HSPC071 protein /FL=gb:AL136633.1 gb:BC001623.1 gb:AF161556.1 gb:NM_014161.1	
209068_at	Consensus includes gb:AA695583 /FEA=EST /DB_XREF=gi:2703730 /DB_XREF=est:z142g07.sl /CLONE=IMAGE:433500 /UG=Hs.42915 ARE2 (actin-related protein 2, yeast) homolog /FL=gb:AF006082.1 gb:NM_005722.1	
46256_at	gb:DB9678.1 /DEF=Homo sapiens mRNA for A-U-rich element RNA binding factor, complete cds. /FEA=mrna /PROD=A-U-rich element RNA binding factor /DB_XREF=gi:3218539 /UG=Hs.170311 heterogeneous nuclear ribonucleoprotein D-like /FL=gb:DB9092.1 gb:DB89678.1	
218068_s_at	Cluster Incl. AA522670.ni39a05.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-979184 /clone_end=3 /gb=AA522670 /gi=2263382 /ug=Hs.7247 /len=684	
208843_s_at	gb:NM_024836.1 /DEF=Homo sapiens hypothetical protein FLJ22301 (FLJ22301), mRNA. /FEA=mrna /GEN=FLJ22301 /PROD=hypothetical protein FLJ22301 /DB_XREF=gi:13376246 /UG=Hs.181406 hypothetical protein FLJ22301 /FL=gb:NM_024836.1	
202869_at	gb:BC001408.1 /DEF=Homo sapiens, clone MGC1233, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC1233) /DB_XREF=gi:12655112 /UG=Hs.6880 DKFZP434D156 protein /FL=gb:BC001408.1	
213546_at	gb:NM_016816.1 /DEF=Homo sapiens 2,5-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E18, mRNA. /FEA=mrna /GEN=OAS1 /PROD=2,5-oligoadenylate synthetase 1, isoform E18 /DB_XREF=gi:8051620 /UG=Hs.82396 2,5-oligoadenylate synthetase 1 (40-46 kD) /FL=gb:NM_016816.1	
214789_x_at	Consensus includes gb:AL050378.1 /DEF=Homo sapiens mRNA, cDNA DKFZp586t1420 (from clone DKFZp586t1420); partial cds. /FEA=mrna /GEN=DKFZp586t1420 /PROD=hypothetical protein /DB_XREF=gi:4914581 /UG=Hs.112423 Homo sapiens mRNA; cDNA DKFZp586t1420 (from clone DKFZp586t1420); partial cds	
213649_at	Consensus includes gb:AA524274 /FEA=EST /DB_XREF=gi:2265202 /DB_XREF=est:ng34d08.sl /CLONE=IMAGE:936687 /UG=Hs.155160 Splicing factor, arginineserine-rich, 46kD	
212251_at	Consensus includes gb:AA524053 /FEA=EST /DB_XREF=gi:2264981 /DB_XREF=est:ng33b07.sl /CLONE=IMAGE:936565 /UG=Hs.184167 splicing factor, arginineserine-rich 7 (35kD)	
209166_s_at	Consensus includes gb:AI972475 /FEA=EST /DB_XREF=gi:5769391 /DB_XREF=est:wr40b09.x1 /CLONE=IMAGE:2490137 /UG=Hs.243901 Homo sapiens cDNA conjugating enzyme E2L 3 /FL=gb:NM_003347.1	
200683_s_at	FLJ20738 f18, clone HEP08257	
219913_s_at	gb:U68567.1 /DEF=Human lysosomal acid alpha-mannosidase mRNA, complete cds. /FEA=mrna /PROD=lysosomal acid alpha-mannosidase /DB_XREF=gi:1658373 /UG=Hs.279854 mannosidase, alpha, class 2B, member 1 /FL=gb:NM_000528.1 gb:BC000736.1 gb:U05572.1 gb:U068567.1	
218104_at	gb:U060266.1	
	Consensus includes gb:89564689 /FEA=EST /DB_XREF=gi:11766267 /DB_XREF=est:601658226R1 /CLONE=IMAGE:3885630 /UG=Hs.108104 ubiquitin-conjugating enzyme E2L 3	
	gb:NM_016652.2 /DEF=Homo sapiens CGI-201 protein (LOC51340), mRNA. /FEA=mrna /GEN=LOC51340 /PROD=CGI-201 protein /DB_XREF=gi:11072090	
	gb:NM_016652.2 /DEF=Homo sapiens crooked neck protein (crn) /FL=gb:AF255443.2 gb:NM_016652.2 gb:AF318302.1	
	gb:NM_017746.1 /DEF=Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA. /FEA=mrna /GEN=FLJ20287 /PROD=hypothetical protein FLJ20287 /DB_XREF=gi:8923268 /UG=Hs.26369 hypothetical protein FLJ20287 /FL=gb:NM_017746.1	

212345_s_at	Consensus includes gb:BE675139 /FEA=EST /DB_XREF=gi:10035680 /DB_XREF=est:f03b12.x1 /CLONE=IMAGE:3293567 /UG=Hs.13659 hypothetical protein DKFZ586F2423
213982_s_at	Consensus includes gb:EG107203 /FEA=EST /DB_XREF=gi:12601049 /DB_XREF=est:602290933F1 /CLONE=IMAGE:4385577 /UG=Hs.242271 KIAA0471 gene product
202519_at	gb:NM_014938.1 /DEF=Homo sapiens KIAA0867 protein (MONDOA), mRNA. /FEA=mrna /GEN=MONDOA /PROD=MONDOA protein /DB_XREF=gi:7662347 /UG=Hs.52081 KIAA0867 protein /FL=gb:AB020674.1 gb:NM_014938.1
202892_at	gb:NM_004661.1 /DEF=Homo sapiens CDC23 (cell division cycle 23, yeast, homolog) /CDC23, mRNA. /FEA=mrna /GEN=CDC23 /PROD=cell division cycle 23, yeast homolog; CDC23 /DB_XREF=gi:4757947 /UG=Hs.153546 CDC23 (cell division cycle 23, yeast, homolog) /FL=gb:AF053977.1 gb:AB011472.1 gb:NM_004661.1 gb:AF191341.1
213876_x_at	Consensus includes gb:AW089584 /FEA=EST /DB_XREF=gi:6046928 /DB_XREF=est:x020f04.x1 /CLONE=IMAGE:2594335 /UG=Hs.171909 U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2
202054_s_at	gb:NM_000382.1 /DEF=Homo sapiens aldehyde dehydrogenase 3 family, member A2 (ALDH3A2), mRNA. /FEA=mrna /GEN=ALDH3A2 /PROD=aldehyde dehydrogenase 3A2 /DB_XREF=gi:4557302 /UG=Hs.159608 aldehyde dehydrogenase 3 family, member A2 /FL=gb:L47162.1 gb:U46689.1 gb:NM_000382.1
217776_at	gb:AF167438.1 /DEF=Homo sapiens androgen-regulated short-chain dehydrogenasereductase 1 (ARSDR1) mRNA, complete cds. /FEA=mrna /GEN=ARSDR1 /PROD=androgen-regulated short-chain dehydrogenasereductase 1 /DB_XREF=gi:9622123 /UG=Hs.179817 CQI-82 protein /FL=gb:BC000112.1
208758_at	gb:AF151840.1 gb:NM_016026.1 gb:AF167438.1
212749_s_at	Consensus includes gb:AT096477 /FEA=EST /DB_XREF=gi:3445971 /DB_XREF=est:ga03c06.x1 /CLONE=IMAGE:1685674 /UG=Hs.48297 DKFZ586C1620 protein ribonucleotide formyltransferaseTMP cyclohydrolase /FL=gb:U37436.1 gb:D82348.1 gb:D89976.1 gb:NM_004044.1
200890_s_at	Consensus includes gb:AW006345 /FEA=EST /DB_XREF=gi:5855123 /DB_XREF=est:wt04d05.x1 /CLONE=IMAGE:2506473 /UG=Hs.250773 signal sequence receptor, alpha (translocase-associated protein alpha) /FL=gb:AF15965.1 gb:NM_003144.2
211675_s_at	gb:AF054589.1 /DEF=Homo sapiens HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds. /FEA=mrna /PROD=HIC protein isoform p32; HIC protein isoform p40 /DB_XREF=gi:3426297 /FL=gb:AF054589.1
206792_x_at	gb:NM_000923.1 /DEF=Homo sapiens phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) (PDE4C), mRNA. /FEA=mrna /GEN=PDE4C /PROD=phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) /DB_XREF=gi:4505664 /UG=Hs.189 phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) /FL=gb:NM_000923.1
218718_at	gb:NM_016205.1 /DEF=Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /FEA=mrna /GEN=PDGFC /PROD=secretory growth factor-like protein fallotelin /DB_XREF=gi:9994186 /UG=Hs.43080 platelet derived growth factor C /FL=gb:AF091434.1 gb:AF244813.1 gb:AB033831.1
201742_x_at	gb:NM_006924.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA. /FEA=mrna /GEN=SFRS1 /PROD=splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /DB_XREF=gi:5902075 /UG=Hs.73737 splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /FL=gb:M69040.1 gb:NM_006924.1
218622_at	gb:NM_024057.1 /DEF=Homo sapiens hypothetical protein MGC5585 (MGC5585), mRNA. /FEA=mrna /GEN=MGC5585 /PROD=hypothetical protein MGC5585 /DB_XREF=gi:13129027 /UG=Hs.5152 hypothetical protein MGC5585 /FL=gb:BC000861.1 gb:NM_024057.1
212176_at	Consensus includes gb:AA902326 /FEA=EST /DB_XREF=gi:3037233 /DB_XREF=est:ok92b01.s1 /CLONE=IMAGE:1521385 /UG=Hs.18368 DKFZ584B0769 protein
218970_s_at	gb:NM_015960.1 /DEF=Homo sapiens CGI-32 protein (LOC51076), mRNA. /FEA=mrna /GEN=LOC51076 /PROD=CGI-32 protein /DB_XREF=gi:7705727 /UG=Hs.16606 CGI-32 protein /FL=gb:AF132966.1 gb:NM_015960.1
201696_at	gb:NM_005626.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 4 (SFRS4), mRNA. /FEA=mrna /GEN=SFRS4 /PROD=splicing factor, arginineserine-rich 4 /DB_XREF=gi:5032088 /UG=Hs.76122 splicing factor, arginineserine-rich 4 /FL=gb:BC002781.1 gb:L14076.1 gb:NM_005626.1
222103_at	Consensus includes gb:AI434345 /FEA=EST /DB_XREF=gi:4255529 /DB_XREF=est:t148b06.x1 /CLONE=IMAGE:2133683 /UG=Hs.36908 activating transcription factor 1 /FL=gb:NM_005171.1
204036_at	Consensus includes gb:AW269335 /FEA=EST /DB_XREF=gi:6656365 /DB_XREF=est:xs47d05.x1 /CLONE=IMAGE:2772777 /UG=Hs.75794 endothelial differentiation factor 1 /FL=gb:NM_005171.1
218283_at	Consensus includes gb:AW269335 /FEA=EST /DB_XREF=gi:6656365 /DB_XREF=est:xs47d05.x1 /CLONE=IMAGE:2772777 /UG=Hs.75794 endothelial differentiation factor, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1
209654_at	gb:NM_016305.1 /DEF=Homo sapiens klaa-iso protein (LOC51188), mRNA. /FEA=mrna /GEN=LOC51188 /PROD=klaa-iso protein /DB_XREF=gi:10047103 /UG=Hs.9774 klaa-iso protein /FL=gb:NM_016305.1 gb:AF201950.1
	gb:BC004902.1 /DEF=Homo sapiens, clone MGC:4271, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:4271) /DB_XREF=gi:13436178 /UG=Hs.5070 KIAA0947 protein /FL=gb:BC004902.1

209083_at	gb:U34690.1 /DEF=Human coronin-like protein (HCOROL) mRNA, complete cds. /FEA=mrna /GEN=HCOROL /PROD=coronin-like protein /DB_XREF=gi:1002922 /UG=Hs.109606 coronin, actin-binding protein, 1A /FL=gb:U34690.1 gb:NM_007074.1 gb:D44497.1
221873_at	Consensus includes gb:AW162015 /FEA=EST /DB_XREF=gi:6301048 /DB_XREF=est:au72409.x1 /CLONE=IMAGE:2781809 /UG=Hs.154095 zinc finger protein 143 (clone pH2-1)
213573_at	Consensus includes gb:AA861608 /FEA=EST /DB_XREF=gi:2953748 /DB_XREF=est:ak34601.s1 /CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (Im-porin) beta 1
209580_s_at	gb:AF114784.1 /DEF=Homo sapiens methyl-CpG binding endonuclease (MED1) mRNA, complete cds. /FEA=mrna /GEN=MED1 /PROD=methyl-CpG binding endonuclease /DB_XREF=gi:4539758 /UG=Hs.35947 methyl-CpG binding domain protein 4 /FL=gb:AF072250.1 gb:NM_003925.1 gb:AF114784.1
219097_x_at	gb:NM_024104.1 /DEF=Homo sapiens hypothetical protein MGC2747 (MGC2747), mRNA. /FEA=mrna /GEN=MGC2747 /PROD=hypothetical protein MGC2747 /DB_XREF=gi:13129111 /UG=Hs.227203 hypothetical protein MGC2747 /FL=gb:BC001680.1 gb:BC001948.1 gb:NM_024104.1
206513_at	gb:NM_004833.1 /DEF=Homo sapiens absent in melanoma 2 (AIM2), mRNA. /FEA=mrna /GEN=AIM2 /PROD=absent in melanoma 2 /DB_XREF=gi:4757733 /UG=Hs.105115 absent in melanoma 2 /FL=gb:AF024714.1 gb:NM_004833.1
209268_at	gb:AF165513.1 /DEF=Homo sapiens vacuolar protein sorting 45B (yeast homolog) /FL=gb:NM_007259.1 gb:AF165513.1
219329_s_at	gb:AF165513.1 /DEF=Homo sapiens vacuolar protein sorting 45B (yeast homolog) /FL=gb:NM_007259.1 gb:AF165513.1
202051_s_at	gb:NM_016085.1 /DEF=Homo sapiens apoptosis related protein APR-3 (APR-3), mRNA. /FEA=mrna /GEN=APR-3 /PROD=apoptosis related protein APR-3 /DB_XREF=gi:7706360 /UG=Hs.9527 apoptosis related protein APR-3 /FL=gb:AF144055.2 gb:NM_016085.1
2020749_at	gb:NM_005095.1 /DEF=Homo sapiens zinc finger protein 262 (ZNF262), mRNA. /FEA=mrna /GEN=ZNF262 /PROD=zinc finger protein 262 /DB_XREF=gi:4827068 /
213373_s_at	gb:NM_005095.1 /DEF=Homo sapiens zinc finger protein 262 (ZNF262), mRNA. /FEA=mrna /GEN=ZNF262 /PROD=zinc finger protein 262 /DB_XREF=gi:4827068 /
212673_at	gb:NM_150390 zinc finger protein 262 /FL=gb:AB007885.1 gb:NM_005095.1
201771_at	Consensus includes gb:BF112006 /FEA=EST /DB_XREF=gi:10941619 /DB_XREF=est:7137e05.x1 /CLONE=IMAGE:3523665 /UG=Hs.10842 RAN, member RAS oncogene family /
209607_x_at	FL=gb:BC000852.1 gb:BC004272.1 gb:K31469.1 gb:AF052578.1 gb:AF054189.1 gb:NM_006325.2
217317_s_at	Consensus includes gb:BF439983 /FEA=EST /DB_XREF=gi:11432500 /DB_XREF=est:nac51f11.x1 /CLONE=IMAGE:3406220 /UG=Hs.19949 caspase 8, apopto-sis-related
202272_s_at	cysteine protease /FL=gb:U58143.1
210629_x_at	Consensus includes gb:D42084.1 /DEF=Human mRNA for KIAA0094 gene, partial cds. /FEA=mrna /GEN=KIAA0094 /PROD=secretory carrier membra- ne protein 3 /DB_XREF=gi:5032076 /UG=Hs.200600 secretory carrier membrane protein 3 /FL=gb:BC000161.2 gb:BC005135.1 gb:AF005039.1
205329_s_at	gb:NM_005698.1 /DEF=Homo sapiens secretory carrier membrane protein 3 (SCAMP3), mRNA. /FEA=mrna /GEN=SCAMP3 /PROD=secretory carrier membra- ne protein 3 /DB_XREF=gi:5032076 /UG=Hs.200600 secretory carrier membrane protein 3 /FL=gb:BC000161.2 gb:BC005135.1 gb:AF005039.1
218194_at	gb:NM_005698.1 /DEF=Homo sapiens secretory carrier membrane protein 3 (SCAMP3), mRNA. /FEA=mrna /GEN=SCAMP3 /PROD=secretory carrier membra- ne protein 3 /DB_XREF=gi:5032076 /UG=Hs.200600 secretory carrier membrane protein 3 /FL=gb:BC000161.2 gb:BC005135.1 gb:AF005039.1
220560_at	gb:U08032.1 /DEF=Human thermolabile (monamine, M form) phenol sulfotransferase (STM) mRNA, complete cds. /FEA=mrna /GEN=STM /PROD=thermolabile (monamine, M form) phenol sulfotransferase /DB_XREF=gi:468256 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-prefering, member 3 /FL=gb:NM_003166.1 gb:U19956.1 gb:U34199.1 gb:U08032.1
208270_s_at	Consensus includes gb:AB002391.2 /DEF=Homo sapiens mRNA for KIAA0393 protein, partial cds. /FEA=mrna /GEN=KIAA0393 /PROD=KIAA0393 protein /DB_XREF=gi:6683696 /UG=Hs.266933 hct domain and RLD 2
220175_s_at	gb:NM_015176.1 /DEF=Homo sapiens KIAA0483 protein (KIAA0483), mRNA. /FEA=mrna /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:7662157 /UG=Hs.64691 KIAA0483 protein /FL=gb:NM_015176.1
212429_s_at	gb:AF000425.1 /DEF=Homo sapiens LST1 mRNA, CLSTIA splice variant, complete cds. /FEA=mrna /GEN=LST1 /DB_XREF=gi:2145065 /UG=Hs.88411
205329_s_at	Lymphocyte antigen 117 /FL=gb:AF000425.1
218194_at	gb:NM_003794.1 /DEF=Homo sapiens sorting nexin 4 (SNX4), mRNA. /FEA=mrna /GEN=SNX4 /PROD=sorting nexin 4 /DB_XREF=gi:4507144 /UG=Hs.267812
220560_at	gb:NM_003794.1 /DEF=Homo sapiens sorting nexin 4 (SNX4), mRNA. /FEA=mrna /GEN=SNX4 /PROD=sorting nexin 4 /DB_XREF=gi:4507144 /UG=Hs.267812
208270_s_at	sorting nexin 4 /FL=gb:AF130078.1 gb:AF065485.1 gb:NM_003794.1
220175_s_at	gb:NM_015523.1 /DEF=Homo sapiens small fragment nuclelease (DKFZP566E144), mRNA. /FEA=mrna /GEN=DKFZP566E144 /PROD=small fragment nuclelease /DB_XREF=gi:7661645 /UG=Hs.7527 small fragment nuclelease /FL=gb:AF151872.1 gb:AL110239.1 gb:NM_015523.1
212429_s_at	gb:NM_014144.1 /DEF=Homo sapiens SNX3 protein (SNX3), mRNA. /FEA=mrna /GEN=SNX3 /PROD=SNX3 protein /DB_XREF=gi:7662662 /UG=Hs.272100 SNX3 protein /FL=gb:AB029488.1 gb:NM_014144.1
208270_s_at	gb:NM_020216.2 /DEF=Homo sapiens arginyl aminopeptidase (aminopeptidase B) (RUPPEP), mRNA. /FEA=mrna /GEN=RUPPEP /PROD=arginyl aminopepti- dase (aminopeptidase B) /DB_XREF=gi:1344030 /UG=Hs.283667 arginyl aminopeptidase (aminopeptidase B) /FL=gb:NM_020216.2
220175_s_at	gb:NM_020667.1 /DEF=Homo sapiens hypothetical protein from clone 1659351 (LOC57397), mRNA. /FEA=mrna /GEN=LOC57397 /PROD=hypothetical protein from clone 1659351 /DB_XREF=gi:10190707 /UG=Hs.288838 hypothetical protein from clone 1659351 /FL=gb:NM_020667.1
212429_s_at	Consensus includes gb:AW194657 /FEA=EST /DB_XREF=gi:6473557 /DB_XREF=est:x528b12.x1 /CLONE=IMAGE:2577599 /UG=Hs.75782 general transcription factor IIIC, polypeptide 2 (beta subunit, 110KD)

209058_at	gb:AB002282.1 / DEF=Homo sapiens mRNA for hMEF1alpha, complete cds. / FEA=mrna / PROD=hMEF1alpha / DB_XREF=gi:6526354 / UG=Hs.174050 endothelial differentiation-related factor 1 / FL=gb:NM_003792.1 gb:AB002282.1
21212535_at	Consensus includes gb:AA142929 / FEA=EST / DB_XREF=gi:1712307 / DB_XREF=est:z140g07.s1 / CLONE=IMAGE:504444 / UG=Hs.288993 ESTs gb:NM_003348.1 / DEF=Homo sapiens ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA. / FEA=mrna / GEN=UBE2N / PROD=ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) / DB_XREF=gi:4507792 / UG=Hs.75355 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) / FL=gb:DB3004.1 gb:BC000396.1 gb:BC003365.1 gb:NM_003348.1
2201524_x_at	gous to yeast UBE13) / PROD=sorting nexin 1 (SNX1), mRNA. / FEA=mrna / GEN=SNX1 / PROD=sorting nexin 1 / DB_XREF=gi:4507138 / UG=Hs.75283 gb:NM_003099.1 / DEF=Homo sapiens sorting nexin 1 (SNX1), mRNA. / FEA=mrna / GEN=SNX1 / PROD=sorting nexin 1 / DB_XREF=gi:4507138 / UG=Hs.75283
2201716_at	sorting nexin 1 / FL=gb:BC000357.1 gb:U53225.1 gb:AF065483.1 gb:NM_003099.1 Consensus includes gb:AL338837 / FEA=EST / DB_XREF=gi:4075764 / DB_XREF=est:qg28f09.x1 / CLONE=IMAGE:1933865 / UG=Hs.82254 zotoin related factor
2213097_s_at	1 Consensus includes gb:AL338837 / FEA=EST / DB_XREF=gi:4075764 / DB_XREF=est:qg28f09.x1 / CLONE=IMAGE:1933865 / UG=Hs.82254 zotoin related factor Consensus includes gb:AL338837 / FEA=EST / DB_XREF=gi:4075764 / DB_XREF=est:qg28f09.x1 / CLONE=IMAGE:1933865 / UG=Hs.82254 zotoin related factor
2213532_at	Consensus includes gb:AL338837 / FEA=EST / DB_XREF=gi:4075764 / DB_XREF=est:qg28f09.x1 / CLONE=IMAGE:1933865 / UG=Hs.82254 zotoin related factor Consensus includes gb:AL338837 / FEA=EST / DB_XREF=gi:4075764 / DB_XREF=est:qg28f09.x1 / CLONE=IMAGE:1933865 / UG=Hs.82254 zotoin related factor
2210766_s_at	Consensus includes gb:AK001618.1 / DEF=Homo sapiens cDNA FLJ10756 fis. clone NT2R3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. / FEA=mrna / DB_XREF=gi:7022983 / UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kd / FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1
209523_at	Consensus includes gb:AK001618.1 / DEF=Homo sapiens cDNA FLJ10756 fis. clone NT2R3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. / FEA=mrna / DB_XREF=gi:7022983 / UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kd / FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1
209276_s_at	glutaredoxin (thioltransferase) / FL=gb:BC005304.1 gb:AF162769.1 gb:D21238.1 Consensus includes gb:AA79488 / FEA=EST / DB_XREF=gi:2208044 / DB_XREF=est:zv21c09.s1 / CLONE=IMAGE:754288 / UG=Hs.4113 S-adenosylhomocysteine hydrolase-like 1 / FL=gb:U82761.1 gb:NM_006621.1
200848_at	Consensus includes gb:AB028973.1 / DEF=Homo sapiens mRNA for KIAA1050 protein, partial cds. / FEA=mrna / GEN=KIAA1050 / PROD=KIAA1050 protein / DB_XREF=gi:5689436 / UG=Hs.184628 hypothetical protein FLJ10883
212406_s_at	Consensus includes gb:AL049761 / DEF=Human DNA sequence from clone RPS-863C7 on chromosome 20p12.3-13. Contains the CSNK2A1 gene for casein kinase 2 alpha 1 polypeptide (EC 2.7.1.37), ESTs, STSs and GSSs / FEA=mrna_2 / DB_XREF=gi:5738437 / UG=Hs.155140 casein kinase 2, alpha 1 polypeptide
212072_s_at	gb:NM_014905.1 / DEF=Homo sapiens glutaminase (GLS), mRNA. / FEA=mrna / GEN=GLS / PROD=glutaminase C / DB_XREF=gi:7662327 / UG=Hs.1239189 glutaminase / FL=gb:AB020645.1 gb:AF097493.1 gb:AF23943.1 gb:NM_014905.1
203159_at	gb:NM_014345.1 / DEF=Homo sapiens endocrine regulator (HRIHPB2436), mRNA. / FEA=mrna / GEN=HRIHPB2436 / PROD=endocrine regulator / DB_XREF=gi:7657183 / UG=Hs.48433 endocrine regulator / FL=gb:AF121141.1 gb:NM_014345.1
203521_s_at	gb:NM_006820.1 / DEF=Homo sapiens hypothetical protein, expressed in osteoblast (G53686), mRNA. / FEA=mrna / GEN=G53686 / PROD=hypothetical protein, expressed in osteoblast / DB_XREF=gi:5803026 / UG=Hs.75470 hypothetical protein, expressed in osteoblast / FL=gb:AB000115.1
204439_at	gb:NM_006820.1 / DEF=Homo sapiens hypothetical protein FLJ20534 (FLJ20534), mRNA. / FEA=mrna / GEN=FLJ20534 / PROD=hypothetical protein FLJ20534 / DB_XREF=gi:8923502 / UG=Hs.44344 hypothetical protein FLJ20534 / FL=gb:AL336673.1 gb:NM_017867.1
218646_at	Consensus includes gb:AUI45005 / FEA=EST / DB_XREF=gi:11006526 / DB_XREF=est:AUI45005 / CLONE=HEMAL1003603 / UG=Hs.44450 Sp3 transcription factor
213168_at	gb:BC003092.1 / DEF=Homo sapiens, similar to retinoblastoma binding protein 4, clone MGC:1393, mRNA, complete cds. / FEA=mrna / PROD=Similar to retinoblastoma binding protein 4 / DB_XREF=gi:13111850 / UG=Hs.16003 retinoblastoma-binding protein 4 / FL=gb:BC003092.1 gb:NM_005610.1
210371_s_at	gb:NM_004515.1 / DEF=Homo sapiens interleukin enhancer binding factor 2, 45kd (ILF2), mRNA. / FEA=mrna / GEN=ILF2 / PROD=interleukin enhancer binding factor 2, 45kd / DB_XREF=gi:4758601 / UG=Hs.75117 interleukin enhancer binding factor 2, 45kd / FL=gb:BC000382.1 gb:NM_004515.1
200052_s_at	gb:U10323.1 / DEF=Homo sapiens eukaryotic translation initiation factor 1A (EIF1A), mRNA. / FEA=mrna / GEN=EIF1A / PROD=eukaryotic translation initiation factor 1A / DB_XREF=gi:4503498 / UG=Hs.4310 eukaryotic translation initiation factor 1A / FL=gb:BC000793.1 gb:U10323.1
201019_s_at	gb:NM_001412.1 / DEF=Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), mRNA. / FEA=mrna / GEN=TM6SF1 / PROD=transmembrane 6 superfamily member 1 / DB_XREF=gi:13194198 / UG=Hs.13365 transmembrane 6 superfamily member 1 / FL=gb:AF255922.1 gb:NM_023003.1
219892_at	gb:NM_018475.1 / DEF=Homo sapiens uncharacterized hypothetical protein HTMP (LOC55858), mRNA. / FEA=mrna / GEN=LOC55858 / PROD=uncharacterized hypothetical protein HTMP / DB_XREF=gi:8923360 / UG=Hs.236510 uncharacterized hypothetical protein HTMP / FL=gb:BC003545.1 gb:AF220188.1
218095_s_at	gb:NM_018475.1 / DEF=Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), mRNA. / FEA=mrna / GEN=TM6SF1 / PROD=transmembrane 6 superfamily member 1 / DB_XREF=gi:13194198 / UG=Hs.13365 transmembrane 6 superfamily member 1 / FL=gb:AF255922.1 gb:NM_023003.1

218042_at	gb:NM_016129.1 / DEF=Homo sapiens COP9 complex subunit 4 (LOC51138), mRNA. / FEA=mrna / GEN=LOC51138 / PROD=COP9 complex subunit 4 / DB_XREF=gi:7705844 / UG=Hs.6671 / COP9 complex subunit 4 / FL=gb:BC004302.1 gb:AF100757.1 gb:NM_016129.1
202172_at	Consensus includes gb:EG035116 / FEA=EST / DB_XREF=gi:12428927 / DB_XREF=est:602324811P1 / CLONE=IMAGE:4412907 / UG=Hs.6557 zinc finger protein 161 / FL=gb:DB28118.1 gb:NM_007146.1
218108_at	gb:NM_018108.1 / DEF=Homo sapiens hypothetical protein FLJ10483 (FLJ10483), mRNA. / FEA=mrna / GEN=FLJ10483 / PROD=hypothetical protein FLJ10483 / DB_XREF=gi:8922451 / UG=Hs.6877 hypothetical protein FLJ10483 / FL=gb:NM_018108.1
212539_at	Consensus includes gb:AI422099 / FEA=EST / DB_XREF=gi:4268030 / DB_XREF=est:tf57509.x1 / CLONE=IMAGE:2103425 / UG=Hs.14570 hypothetical protein FLJ22530
212635_at	Consensus includes gb:AW161626 / FEA=EST / DB_XREF=gi:6300659 / DB_XREF=est:au68b11.x1 / CLONE=IMAGE:2781405 / UG=Hs.21739 Homo sapiens mRNA; cDNA DKFZp58611518 (from clone DKFZp58611518)
203356_at	Consensus includes gb:BE349584 / FEA=EST / DB_XREF=gi:9261437 / DB_XREF=est:ht55h12.x1 / CLONE=IMAGE:3150695 / UG=Hs.7145 calpain 7 / FL=gb:AB028639.1 gb:NM_014236.1
208174_x_at	gb:NM_005089.1 / DEF=Homo sapiens U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 (U2AF1RS2), mRNA. / FEA=mrna / GEN=U2AF1RS2 / PROD=U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 / FL=gb:D49677.1 gb:NM_005089.1
53912_at	Ribonucleoprotein auxiliary factor, small subunit 2 / FL=gb:D49677.1 gb:NM_005089.1
221736_at	Cluster Incl. AI668643:zb13f10.X5 Homo sapiens cDNA, 3' end / clone=IMAGE-301963 / clone_end=3 / gb=AI668643 / gi=4827951 / ug=Hs.15827 / len=601
209475_at	Consensus includes gb:AA156777 / FEA=EST / DB_XREF=gi:1728392 / DB_XREF=est:z118c08.s1 / CLONE=IMAGE:502286 / UG=Hs.25431 KIAA1219 protein
204366_s_at	gb:AF106069.1 / DEF=Homo sapiens deubiquitinating enzyme (UNPH4) mRNA, complete cds. / FEA=mrna / GEN=UNPH4 / PROD=deubiquitinating enzyme / DB_XREF=gi:5814096 / UG=Hs.23168 ubiquitin specific protease 15 / FL=gb:AF013990.1 gb:AF106069.1
212584_at	gb:NM_001521.1 / DEF=Homo sapiens general transcription factor IIIC, polypeptide 2 (beta subunit, 110KD) (GTF3C2), mRNA. / FEA=mrna / GEN=GTF3C2 / PROD=general transcription factor IIIC, polypeptide 2 (beta subunit, 110KD) / DB_XREF=gi:4504204 / UG=Hs.75782 general transcrip- tion factor IIIC, polypeptide 2 (beta subunit, 110KD) / FL=gb:DI3636.1 gb:NM_001521.1
212140_at	Consensus includes gb:EG260519 / FEA=EST / DB_XREF=gi:12770335 / DB_XREF=est:602372065F1 / CLONE=IMAGE:4480024 / UG=Hs.129952 KIAA0560 gene product
219083_at	Consensus includes gb:AB014548.1 / DEF=Homo sapiens mRNA for KIAA0648 protein, partial cds. / FEA=mrna / GEN=KIAA0648 / PROD=KIAA0648 protein / DB_XREF=gi:3327109 / UG=Hs.31921 KIAA0648 protein
215772_x_at	gb:NM_018130.1 / DEF=Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. / FEA=mrna / GEN=FLJ10539 / PROD=hypothetical protein FLJ10539 / FL=gb:NM_018130.1
216194_s_at	FLJ10539 / DB_XREF=gi:8922499 / UG=Hs.93391 hypothetical protein FLJ10539 / FL=gb:NM_018130.1
204373_s_at	Consensus includes gb:AL050226.1 / DEF=Homo sapiens mRNA; cDNA DKFZp586M2023 (from clone DKFZp586M2023); partial cds. / FEA=mrna / GEN=DKFZp586M2023 / PROD=hypothetical protein / DB_XREF=gi:4884469 / UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
208927_at	Consensus includes gb:AD001527 / DEF=Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence / FEA=CDS_3 / DB_XREF=gi:1905899 / UG=Hs.31053 cytoskeleton-associated protein 1
220146_at	gb:NM_014810.1 / DEF=Homo sapiens KIAA0480 gene product (KIAA0480), mRNA. / FEA=mrna / GEN=KIAA0480 / PROD=KIAA0480 gene product / DB_XREF=gi:7662155 / UG=Hs.92200 KIAA0480 gene product / FL=gb:AB007949.1 gb:NM_014810.1
219694_at	Consensus includes gb:BF673888 / FEA=EST / DB_XREF=gi:11947783 / DB_XREF=est:602137554F1 / CLONE=IMAGE:4274077 / UG=Hs.129951 speckle-type POZ protein / FL=gb:BC001269.1
213229_at	gb:NM_016562.1 / DEF=Homo sapiens toll-like receptor 7 (LOC51284), mRNA. / FEA=mrna / GEN=LOC51284 / PROD=toll-like receptor 7 / DB_XREF=gi:7706092 / UG=Hs.179152 toll-like receptor 7 / FL=gb:AF240467.1 gb:NM_016562.1 gb:AF245702.1
214356_s_at	gb:NM_019018.1 / DEF=Homo sapiens hypothetical protein (FLJ11127), mRNA. / FEA=mrna / GEN=FLJ11127 / PROD=hypothetical protein
213153_at	DB_XREF=gi:9506640 / UG=Hs.91165 hypothetical protein / FL=gb:NM_019018.1
218294_s_at	Consensus includes gb:BE590131 / FEA=EST / DB_XREF=gi:11682455 / DB_XREF=est:nab19e04.x1 / CLONE=IMAGE:3266383 / UG=Hs.87889 helicase-moi
221522_at	Consensus includes gb:AI272899 / FEA=EST / DB_XREF=gi:3895167 / DB_XREF=est:q147c07.x1 / CLONE=IMAGE:1875468 / UG=Hs.3852 KIAA0368 protein
	Consensus includes gb:AB028999.1 / DEF=Homo sapiens mRNA for KIAA1076 protein, partial cds. / FEA=mrna / GEN=KIAA1076 / PROD=KIAA1076 protein / DB_XREF=gi:5689488 / UG=Hs.154525 KIAA1076 protein
	DB_XREF=gi:5689488 / UG=Hs.154525 KIAA1076 protein
	Consensus includes gb:AF267865.1 / DEF=Homo sapiens DC41 mRNA, complete cds. / FEA=mrna / PROD=DC41 / DB_XREF=gi:12006056 / UG=Hs.271623 nucleoporin 50KD
	gb:AF267865.1 gb:AF107840.1 gb:NM_007172.1 gb:AF116624.1
	FL=gb:AF267865.1 gb:AF107840.1 gb:NM_007172.1 gb:AF116624.1
	gb:AL136784.1 / DEF=Homo sapiens mRNA; cDNA DKFZp434L0718 (from clone DKFZp434L0718); complete cds. / FEA=mrna / GEN=DKFZp434L0718 / PROD=hypothetical



	protein /DB_XREF=gi:12053080 /UG=Hs.59236 Homo sapiens mRNA; cDNA DKFp434L0718 (from clone DKFp434L0718); complete cds /FL=gb:AL1136784.1 /GEN=GF2EL /
205930_at	gb:NM_005513.1 /DEF=Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2EL), mRNA. /FEA=mRNA /PROD=general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) /FL=gb:NM_005513.1
210312_s_at	gb:BC002640.1 /DEF=Homo sapiens, similar to uterine protein, clone MGC:4279, mRNA, complete cds. /FEA=mRNA /PROD=similar to uterine protein /DB_XREF=gi:12803610 /UG=Hs.4187 hypothetical protein 24636 /FL=gb:BC002640.1
211838_at	Consensus includes gb:AA191426 /FEA=EST /DB_XREF=gi:1780105 /DB_XREF=est:zp83g09.s1 /CLONE=IMAGE:626848 /UG=Hs.279886 RAN binding protein 9 /gb:NM_000249.1 /DEF=Homo sapiens mtL (E. coli) homolog 1 (colon cancer, nonpolar type 2) (MLH1), mRNA. /FEA=mRNA /GEN=MLH1 /PROD=mtL homolog 1 /DB_XREF=gi:4557736 /UG=Hs.57301 mutL (E. coli) homolog 1 (colon cancer, nonpolar type 2) /FL=gb:NM_000249.1 gb:U07343.1
202520_s_at	gb:U07418.1
221834_at	Consensus includes gb:AV700132 /FEA=EST /DB_XREF=gi:10302103 /DB_XREF=est:AV700132 /CLONE=GKGS03 /UG=Hs.295923 seven in absentia (Drosophila) homolog 1
210942_s_at	gb:AB022918.1 /DEF=Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds. /FEA=mRNA /GEN=ST3Gal VI /PROD=alpha2,3-sialyltransferase ST3Gal VI /DB_XREF=gi:4827246 /UG=Hs.34578 alpha2,3-sialyltransferase /FL=gb:AB022918.1
202396_at	gb:NM_006706.1 /DEF=Homo sapiens transcription factor CAL50 (CAL50), mRNA. /FEA=mRNA /GEN=CAL50 /PROD=transcription factor CAL50 /DB_XREF=gi:5729753 /UG=Hs.13063 transcription factor CAL50 /FL=gb:AF017789.1 gb:NM_006706.1
219598_s_at	gb:NM_016104.1 /DEF=Homo sapiens PTD013 protein (PTD013), mRNA. /FEA=mRNA /GEN=PTD013 /PROD=PTD013 protein /DB_XREF=gi:770668 /UG=Hs.279857 PTD013 protein /FL=gb:AF092134.1 gb:NM_016104.1
202502_at	gb:NM_000016.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADM /PROD=acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain /FL=gb:NM_000016.1 gb:AF251043.1 /UG=Hs.79158 acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain /FL=gb:BC005377.1 gb:NM_000016.1 gb:AF251043.1
211968_s_at	Consensus includes gb:AI962933 /FEA=EST /DB_XREF=gi:5755646 /DB_XREF=est:wt25a07.x1 /CLONE=IMAGE:2508468 /UG=Hs.289088 heat shock 90kD protein 1, alpha /FL=gb:NM_005348.1
218027_at	gb:NM_014175.1 /DEF=Homo sapiens HSPC145 protein (HSPC145), mRNA. /FEA=mRNA /GEN=HSPC145 /PROD=HSPC145 protein /DB_XREF=gi:7661805 /UG=Hs.18349 HSPC145 protein /FL=gb:AI136665.1 gb:BC000891.1 gb:AF161494.1 gb:NM_014175.1
217792_at	gb:NM_014426.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mRNA /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657598 /UG=Hs.13794 sorting nexin 5 /FL=gb:BC000100.1 gb:AF121855.1 gb:NM_014426.1
221036_s_at	gb:NM_031301.1 /DEF=Homo sapiens hypothetical protein DKFp564D0372 (DKFp564D0372), mRNA. /FEA=mRNA /GEN=DKFp564D0372 /PROD=hypothetical protein DKFp564D0372 /DB_XREF=gi:13775223 /FL=gb:NM_031301.1
201723_s_at	gb:U41514.1 /DEF=Human UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase mRNA, complete cds. /FEA=mRNA /PROD=UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase /DB_XREF=gi:1136284 /UG=Hs.80120 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 1 (GalNAc-T1) /FL=gb:U41514.1 gb:NM_020474.2
202351_at	Consensus includes gb:AI093579 /FEA=EST /DB_XREF=gi:3432555 /DB_XREF=est:qb15g06.x1 /CLONE=IMAGE:1696378 /UG=Hs.295726 Integrin, alpha V (vitronectin receptor), alpha polypeptide, antigen CD51 /FL=gb:M14648.1 gb:NM_002210.1
208853_s_at	gb:U118887.1 /DEF=Human calnexin mRNA, complete cds. /FEA=mRNA /PROD=calnexin /DB_XREF=gi:306480 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 /gb:BC003552.1 gb:M94859.1 gb:M94852.1 gb:U10284.1 gb:U118887.1
2113278_at	Consensus includes gb:AW014788 /FEA=EST /DB_XREF=gi:5863545 /DB_XREF=est:UI-H-B10-aae-h-10-0-UI.s1 /CLONE=IMAGE:2709354 /UG=Hs.48802 Homo sapiens clone 23632 mRNA sequence
203447_at	Consensus includes gb:AUI57008 /FEA=EST /DB_XREF=gi:11018529 /DB_XREF=est:AUI57008 /CLONE=PLACE1005711 /UG=Hs.193725 proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 /FL=gb:NM_005047.1
212459_x_at	Consensus includes gb:BF593940 /FEA=EST /DB_XREF=gi:111686264 /DB_XREF=est:nab48f10.x1 /CLONE=IMAGE:3269154 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
218514_at	gb:NM_018149.1 /DEF=Homo sapiens hypothetical protein FLJ10587 (FLJ10587), mRNA. /FEA=mRNA /GEN=FLJ10587 /PROD=hypothetical protein FLJ10587 /DB_XREF=gi:8922539 /UG=Hs.7296 hypothetical protein FLJ10587 /FL=gb:NM_018149.1
212648_at	Consensus includes gb:AL079292.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 48814. /FEA=mRNA /PROD=hypothetical protein FLJ10587 /DB_XREF=gi:8922539 /UG=Hs.7296 hypothetical protein FLJ10587 /FL=gb:NM_018149.1
200708_at	Consensus includes gb:AC007017 /putative RNA helicase A Arabidopsis thaliana /DB_XREF=gi:5102732 /UG=Hs.95665 hypothetical protein FLJ10587 /DB_XREF=gi:8922539 /UG=Hs.7296 hypothetical protein FLJ10587 /FL=gb:NM_018149.1
	tein, similar to (AC007017) putative RNA helicase A Arabidopsis thaliana /DB_XREF=gi:5102732 /UG=Hs.95665 hypothetical protein FLJ10587 /DB_XREF=gi:8922539 /UG=Hs.7296 hypothetical protein FLJ10587 /FL=gb:NM_018149.1
	gb:NM_002080.1 /DEF=Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=GOT2 /PROD=aspartate aminotransferase 2 precursor /DB_XREF=gi:4504068 /UG=Hs.170197 glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) /FL=gb:BC000525.1 gb:M22632.1 gb:NM_002080.1

201064_s_at	gb:NM_003819.2 / DEF=Homo sapiens poly(A)-binding protein, cytoplasmic 4 (inducible form) (PABPC4), mRNA. / FEA=mrna / GEN=PABPC4 / PROD=poly(A)-binding protein, cytoplasmic 4(inducible form) / DB_XREF=gi:6552335 / UG=Hs.169900 poly(A)-binding protein, cytoplasmic 4 (inducible form) / FL=gb:NM_003819.2
218604_at	gb:NM_014319.2 / DEF=Homo sapiens integral inner nuclear membrane protein (MAN1), mRNA. / FEA=mrna / PROD=integral inner nuclear membrane protein / DB_XREF=gi:7706606 / UG=Hs.7256 integral inner nuclear membrane protein / FL=gb:AF112299.2 gb:NM_014319.2
214864_s_at	Consensus includes gb:AK024386.1 / DEF=Homo sapiens cDNA FLJ14324 fis, clone PLACE4000100, highly similar to Homo sapiens hydroxypyruvate reductase (GRHPR) gene. / FEA=mrna / DB_XREF=gi:10436760 / UG=Hs.155742 glyoxylate reductase/hydroxypyruvate reductase
202717_s_at	gb:NM_003903.1 / DEF=Homo sapiens CDC16 (cell division cycle 16, S. cerevisiae, homolog) (CDC16), mRNA. / FEA=mrna / GEN=CDC16 / PROD=CDC16 (cell division cycle 16, S. cerevisiae, homolog) / DB_XREF=gi:4502700 / UG=Hs.1592 CDC16 (cell division cycle 16, S. cerevisiae, homolog) / FL=gb:NM_003903.1 gb:U18291.1
201643_x_at	gb:NM_016604.1 / DEF=Homo sapiens putative zinc finger protein (LOC51780), mRNA. / FEA=mrna / GEN=LOC51780 / PROD=putative zinc finger protein / DB_XREF=gi:7706598 / UG=Hs.24125 putative zinc finger protein / FL=gb:AF251039.1 gb:NM_016604.1
213803_at	Consensus includes gb:BG545463 / FEA=EST / DB_XREF=gi:13544128 / DB_XREF=est:602572695F1 / CLONE=IMAGE:4701118 / UG=Hs.180446 karyopherin (importin) beta 1
204689_at	gb:NM_001529.1 / DEF=Homo sapiens hematopoietically expressed homeobox (HHEX), mRNA. / FEA=mrna / GEN=HHEX / PROD=hematopoietically expressed homeobox / DB_XREF=gi:10835016 / UG=Hs.118651 hematopoietically expressed homeobox / FL=gb:NM_001529.1 gb:L16499.1 gb:NM_002729.1
218228_s_at	gb:NM_025235.1 / DEF=Homo sapiens tankyrase 2 (TNKL), mRNA. / FEA=mrna / GEN=TNKL / PROD=tankyrase 2 / DB_XREF=gi:13376841 / UG=Hs.280776 tankyrase 2 / FL=gb:AF264912.1 gb:AF2329696.1 gb:NM_025235.1 gb:AF342982.1
202918_s_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
212263_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
221825_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
211047_x_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
209798_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
204361_s_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
218127_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
220355_s_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
202930_s_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
203745_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
200597_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
218519_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
203947_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
219002_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
220122_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942
203882_at	gb:AF151853.1 / DEF=Homo sapiens CGI-95 protein mRNA, complete cds. / FEA=mrna / PROD=CGI-95 protein / DB_XREF=gi:4929658 / UG=Hs.107942



3, gamma	FL=gb:M87503.1 gb:NM_006084.1	
212174_at	Consensus includes gb:W02312 /FEA-EST /DB_XREF=gi:1274291 /DB_XREF=est:za06d08.x1 /CLONE=IMAGE:291951 /UG=Hs.171811 adenylate kinase 2 /gb:NM_004175.1 /DEF=Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3), mRNA. /FEA=mrna /GEN=SNRPD3 /PROD=small nuclear ribonucleoprotein D3 polypeptide (18kD) /DB_XREF=gi:4759159 /UG=Hs.1575 small nuclear ribonucleoprotein D3 polypeptide (18kD)	
202567_at	FL=gb:BC000457.1 gb:BC003150.1 gb:NM_004175.1 gb:U15009.1 /FEA=gb:BC000457.1 gb:BC003150.1 gb:NM_004175.1 gb:U15009.1 /FEA=mrna /GEN=NT2 /PROD=Nit protein 2 /DB_XREF=gi:9910459 /UG=Hs.15627 Nit	
218557_at	protein 2 /FL=gb:AF260334.1 gb:AF284574.1 gb:NM_020202.1 /FEA=gb:AF260334.1 gb:AF284574.1 gb:NM_020202.1 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872	
211976_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
201990_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
208956_x_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
213939_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
201198_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
203010_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
218067_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
219077_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
215424_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
219043_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
209313_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
202944_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
208985_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
211656_x_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
209358_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
207431_s_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
213070_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
201111_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	
204370_at	Consensus includes gb:AK076168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 /FEA=mrna /GEN=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101	

202911_at	gb:NM_000179.1 /DEF=Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. /FEA=mrna /GEN=MSH6 /PROD=mutS (E. coli) homolog 6 /DB_XREF=gi:4504190 /UG=Hs.3248 mutS (E. coli) homolog 6 /FL=gb:U28946.1 gb:NM_000179.1 gb:U54777.2
204197_s_at	factor 3 /DB_XREF=gi:4757917 /UG=Hs.170019 runt-related transcription factor 3 (RUNX3), mRNA. /FEA=mrna /GEN=RUNX3 /PROD=runt-related transcription factor 3 /FL=gb:NM_004350.1
217809_at	gb:NM_014038.1 /DEF=Homo sapiens HSPC028 protein (HSPC028), mRNA. /FEA=mrna /GEN=HSPC028 /PROD=HSPC028 protein /DB_XREF=gi:7661743 /UG=Hs.5216 HSPC028 protein /FL=gb:AF110323.1 gb:BC003056.1 gb:AF083246.1 gb:NM_014038.1
201054_at	Consensus includes gb:BE565599 /FEA=EST /DB_XREF=gi:11772191 /DB_XREF=est:601660283R1 /CLONE=IMAGE:3906044 /UG=Hs.77492 heterogeneous nuclear ribonucleoprotein A0 /FL=gb:BC001008.1 gb:NM_006805.1 gb:U23803.1
200994_at	Consensus includes gb:BG291787 /FEA=EST /DB_XREF=gi:13050002 /DB_XREF=est:602386007F1 /CLONE=IMAGE:4515240 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1
201572_x_at	gb:NM_001921.1 /DEF=Homo sapiens dCMP deaminase (DCTD), mRNA. /FEA=mrna /GEN=DCTD /PROD=dCMP deaminase /DB_XREF=gi:4503276 /UG=Hs.76894 dCMP deaminase /FL=gb:L12136.1 gb:NM_001921.1
218195_at	gb:NM_024573.1 /DEF=Homo sapiens hypothetical protein FLJ12910 (FLJ12910), mRNA. /FEA=mrna /GEN=FLJ12910 /PROD=hypothetical protein FLJ12910 /DB_XREF=gi:13375745 /UG=Hs.15929 hypothetical protein FLJ12910 /FL=gb:NM_024573.1
219905_at	gb:NM_018538.1 /DEF=Homo sapiens hypothetical protein PRO2801 (PRO2801), mRNA. /FEA=mrna /GEN=PRO2801 /PROD=hypothetical protein PRO2801 /DB_XREF=gi:8924201 /UG=Hs.181223 hypothetical protein PRO2801 /FL=gb:AF119899.1 gb:NM_018538.1
209362_at	Consensus includes gb:AF688580 /FEA=EST /DB_XREF=gi:489874 /DB_XREF=est:wd39h05.xl /CLONE=IMAGE:2330553 /UG=Hs.286145 SRB7 (suppressor of RNA polymerase B, yeast) homolog /FL=gb:U46837.1 gb:U52960.1 gb:NM_004264.1
203983_at	gb:NM_005999.1 /DEF=Homo sapiens translin-associated factor X (TSNAX), mRNA. /FEA=mrna /GEN=TSNAX /PROD=translin-associated factor X /DB_XREF=gi:5174730 /UG=Hs.96247 translin-associated factor X /FL=gb:NM_005999.1
212074_at	Consensus includes gb:BE972774 /FEA=EST /DB_XREF=gi:10586110 /DB_XREF=est:601652004F1 /CLONE=IMAGE:3935281 /UG=Hs.7531 KIAA0810 protein /GB:NM_013229.1 /DEF=Homo sapiens apoptotic protease activating factor (APAF1), transcript variant 1, mRNA. /FEA=mrna /GEN=APAF1 /PROD=apoptotic protease activating factor isoform 1 /DB_XREF=gi:7108332 /UG=Hs.77579 apoptotic protease activating factor
204859_s_at	FL=gb:AB007873.1 gb:AF134397.1 gb:NM_013229.1
205707_at	gb:NM_014339.1 /DEF=Homo sapiens interleukin 17 receptor (IL17R), mRNA. /FEA=mrna /GEN=IL17R /PROD=interleukin 17 receptor /DB_XREF=gi:7657229 /UG=Hs.129751 interleukin 17 receptor /FL=gb:U58917.1 gb:NM_014339.1
218716_x_at	gb:NM_014123.1 /DEF=Homo sapiens CGI-02 protein (CGI-02), mRNA. /FEA=mrna /GEN=CGI-02 /PROD=CGI-02 protein /DB_XREF=gi:6912299 /UG=Hs.33979 CGI-02 protein /FL=gb:AF139422.1 gb:AF13937.1 gb:NM_014123.1
217940_s_at	gb:NM_018210.1 /DEF=Homo sapiens hypothetical protein FLJ10769 (FLJ10769), mRNA. /FEA=mrna /GEN=FLJ10769 /PROD=hypothetical protein FLJ10769 /DB_XREF=gi:8922653 /UG=Hs.8083 hypothetical protein FLJ10769 /FL=gb:AF151071.1 gb:NM_018210.1
219802_at	gb:NM_024854.1 /DEF=Homo sapiens hypothetical protein FLJ22028 (FLJ22028), mRNA. /FEA=mrna /GEN=FLJ22028 /PROD=hypothetical protein FLJ22028 /DB_XREF=gi:13376278 /UG=Hs.192570 hypothetical protein FLJ22028 /FL=gb:NM_024854.1
209359_s_at	gb:AF020043.1 /DEF=Homo sapiens chromosome-associated polypeptide (HCAP) mRNA, complete cds. /FEA=mrna /GEN=HCAP /PROD=chromosome-associated polypeptide /DB_XREF=gi:3089367 /UG=Hs.24485 chondroitin sulfate proteoglycan 6 (bamacan) /FL=gb:AF020043.1 gb:NM_005445.1 gb:AF067163.1
212037_at	Consensus includes gb:BE508848 /FEA=EST /DB_XREF=gi:11592146 /DB_XREF=est:U1-H-B14-aor-e-06-0-UI.s1 /CLONE=IMAGE:3085907 /UG=Hs.44499 pinin, desmosome associated protein
211063_s_at	gb:BC006403.1 /DEF=Homo sapiens, NCK adaptor protein 1, clone MGC:12668, mRNA, complete cds. /FEA=mrna /PROD=NCK adaptor protein 1 /DB_XREF=gi:13623576 /FL=gb:BC006403.1
203791_at	gb:NM_005509.2 /DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA. /FEA=mrna /GEN=DMXL1 /PROD=Dmx-like 1 /DB_XREF=gi:9961348 /UG=Hs.181042 Dmx-like 1 /FL=gb:NM_005509.2
203405_at	gb:NM_003720.1 /DEF=Homo sapiens Down syndrome critical region gene 2 (DSCR2), mRNA. /FEA=mrna /GEN=DSCR2 /PROD=Down syndrome critical region protein 2 /DB_XREF=gi:4505022 /UG=Hs.5198 Down syndrome critical region gene 2 /FL=gb:BC003619.1 gb:NM_003720.1
201604_s_at	gb:NM_002480.1 /DEF=Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA. /FEA=mrna /GEN=MYPT1 /PROD=myosin phosphatase target subunit 1 /DB_XREF=gi:4505316 /UG=Hs.16533 myosin phosphatase, target subunit 1 /FL=gb:NM_002480.1
218348_s_at	gb:NM_014153.1 /DEF=Homo sapiens HSPC055 protein (HSPC055), mRNA. /FEA=mrna /GEN=HSPC055 /PROD=HSPC055 protein /DB_XREF=gi:7661761 /UG=Hs.17989 HSPC055 protein /FL=gb:AF161540.1 gb:NM_014153.1
205659_at	gb:NM_014707.1 /DEF=Homo sapiens histone deacetylase 7B (HDAC7B-PENDING), mRNA. /FEA=mrna /GEN=HDAC7B-PENDING /PROD=histone deacetylase 7B /DB_XREF=gi:7662279 /UG=Hs.116753 histone deacetylase 7B /FL=gb:AB018287.1 gb:NM_014707.1
202268_s_at	gb:NM_003905.1 /DEF=Homo sapiens amyloid beta precursor protein-binding protein 1, 59KD (APBP1), mRNA. /FEA=mrna /GEN=APBP1 /PROD=amyloid beta precursor protein-binding protein 1, 59KD (APBP1) /DB_XREF=gi:4502168 /UG=Hs.61828 amyloid beta precursor protein-binding protein 1,

59kd	FL-gb:AL136798.1 gb:BC000480.1 gb:U0939.1 gb:NM_003905.1	
	gb:NM_005829.1 /DEF=Homo sapiens adaptor-related protein complex 3, sigma 2 subunit (AP3S2), mRNA. /FEA=mrna /GEN=AP3S2 /PROD=adaptor-related protein complex 3, sigma 2 subunit /DB_XREF=gi:5031580 /UG=Hs.154782 adaptor-related protein complex 3, sigma 2 subunit	
202399_s_at	/FL-gb:BC002785.1 gb:NM_005829.1	
	gb:NM_005829.1 /DEF=Homo sapiens hypothetical protein (LOC513325), mRNA. /FEA=mrna /GEN=LOC513325 /PROD=hypothetical protein	
218515_at	/DB_XREF=gi:7706175 /UG=Hs.28461 hypothetical protein /FL-gb:AF208862.1 gb:NM_016631.1	
	gb:U49245.1 /DEF=human geranylgeranyl transferase type II beta-subunit mRNA, complete cds. /FEA=mrna /PROD=geranylgeranyl transferase type II beta-subunit /DB_XREF=gi:1216503 /UG=Hs.78948 Tab geranylgeranyltransferase, beta subunit /FL-gb:U49245.1 gb:NM_004582.1	
209180_at	II beta-subunit /DB_XREF=gi:1216503 /UG=Hs.78948 Tab geranylgeranyltransferase, beta subunit (MAN2A1), mRNA. /FEA=mrna /GEN=MAN2A1 /PROD=mannosidase, alpha, class 2A, member 1 /FL-gb:U31520.1 gb:NM_002372.1 gb:D63998.1	
205105_at	gb:NM_002372.1 /DEF=Homo sapiens mannosidase, alpha, class 2A, member 1 (HSPF1), mRNA. /FEA=mrna /GEN=HSPF1 /PROD=heat shock 40KD protein 1	
	class 2A, member 1 /DB_XREF=gi:4758697 /UG=Hs.32965 mannosidase, alpha, class 2A, member 1 /FL-gb:BC002352.1 gb:NM_006145.1 gb:D49547.1	
200666_s_at	gb:NM_006145.1 /DEF=Homo sapiens heat shock 40KD protein 1 (HSPF1), mRNA. /FEA=mrna /PROD=tetraspan 3 /DB_XREF=gi:12653830	
	/DB_XREF=gi:5453689 /UG=Hs.82646 DnaJ (Hsp40) homolog, subfamily B, member 1 /FL-gb:BC002352.1 gb:NM_005724.1 gb:AF133423.1	
200972_at	gb:BC000704.1 /DEF=Homo sapiens, tetraspan 3, clone MGC:965, mRNA, complete cds. /FEA=mrna /GEN=FLJ10716 /PROD=hypothetical protein	
	/UG=Hs.10090 tetraspan 3 /FL-gb:BC000704.1 gb:BC004280.1 gb:AF054840.1 gb:NM_005724.1 gb:AF133423.1	
218352_at	gb:NM_018191.1 /DEF=Homo sapiens hypothetical protein FLJ10716 (FLJ10716), mRNA. /FEA=mrna /GEN=NM_018191.1	
	FLJ10716 /DB_XREF=gi:8922616 /UG=Hs.61478 hypothetical protein FLJ10716 (FLJ10716), mRNA. /FEA=mrna /GEN=NM_018191.1	
217728_at	gb:NM_014624.2 /DEF=Homo sapiens S100 calcium-binding protein A6 (calyculin) (S100A6), mRNA. /FEA=mrna /GEN=NM_014624.2	
	binding protein A6 /DB_XREF=gi:9845517 /UG=Hs.275243 S100 calcium-binding protein A6 (calyculin) /FL-gb:D87432.1 gb:NM_003983.1	
211971_s_at	Consensus includes gb:AI65308 /FEA=EST /DB_XREF=gi:4737587 /DB_XREF=est:ts21a06.x1 /CLONE=IMAGE:2289202 /UG=Hs.182490 leucine-rich protein	
212500_at	Consensus includes gb:AL049319.1 /DEF=Homo sapiens mRNA; cDNA DKFp5564C046 (from clone DKFp5564C046). /FEA=mrna /DB_XREF=gi:4500092	
218473_s_at	Consensus includes gb:AL049319.1 /DEF=Homo sapiens mRNA; cDNA DKFp5564C046 (from clone DKFp5564C046)	
	gb:NM_024656.1 /DEF=Homo sapiens hypothetical protein FLJ22329 (FLJ22329), mRNA. /FEA=mrna /GEN=FLJ22329 /PROD=hypothetical protein	
203580_s_at	FLJ22329 /DB_XREF=gi:13375904 /UG=Hs.61478 hypothetical protein FLJ22329 (FLJ22329), mRNA. /FEA=mrna /GEN=FLJ22329 /PROD=hypothetical protein	
	gb:NM_003983.1 /DEF=Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 /FL-gb:D87432.1 gb:NM_003983.1	
200900_s_at	/GEN=SLC7A6 /PROD=solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 /FL-gb:D87432.1 gb:NM_003983.1	
	carrier family 7 (cationic amino acid transporter, y+ system), member 6 /FL-gb:D87432.1 gb:NM_003983.1	
221652_s_at	Consensus includes gb:AI583537 /FEA=EST /DB_XREF=gi:4569434 /DB_XREF=est:ts12a03.x1 /CLONE=IMAGE:2228357 /UG=Hs.75709 mannose-6-phosphate	
	receptor (cation dependent) /FL-gb:NM_002355.2 gb:NM16985.1	
217750_s_at	gb:AF274950.1 /DEF=Homo sapiens FNA5-25 mRNA, complete cds. /FEA=mrna /PROD=FNA5-25 /DB_XREF=gi:12751064 /UG=Hs.22595 hypothetical protein	
	FLJ10637 /FL-gb:AF274950.1	
203544_s_at	FLJ10637 /FL-gb:AF274950.1	
221580_s_at	FLJ13855 /	
202629_at	DB_XREF=gi:12751494 /UG=Hs.168232 hypothetical protein FLJ13855 (FLJ13855), mRNA. /FEA=mrna /GEN=FLJ13855 /PROD=hypothetical protein	
	gb:NM_003473.1 /DEF=Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA. /FEA=mrna /GEN=STAM	
205763_s_at	/PROD=signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 /DB_XREF=gi:4507248 /UG=Hs.153487 signal transducing adaptor mole-	
212337_at	cule (SH3 domain and ITAM motif) 1 /FL-gb:U43899.1 gb:NM_003473.1	
212244_at	gb:BC001972.1 /DEF=Homo sapiens, clone MGC:5306, mRNA, complete cds. /FEA=mrna /PROD=unknown (protein for MGC:5306) /DB_XREF=gi:12805036	
222011_s_at	gb:NM_001972.1 /DEF=Homo sapiens, clone MGC:5306, mRNA, complete cds. /FEA=mrna /PROD=unknown (protein for MGC:5306) /DB_XREF=gi:12805036	
204725_s_at	Consensus includes gb:AF681579 /FEA=EST /DB_XREF=gi:10283442 /DB_XREF=est:AV681579 /CLONE=GKBAFE05 /UG=Hs.84084 amyloid beta precursor	
	protein (cytoplasmic tail)-binding protein 2 /FL-gb:AF017782.1 gb:NM_006380.1	
	Consensus includes gb:AF681579 /FEA=EST /DB_XREF=gi:10283442 /DB_XREF=est:AV681579 /CLONE=GKBAFE05 /UG=Hs.84084 amyloid beta precursor	
	protein (cytoplasmic tail)-binding protein 2 /FL-gb:AF017782.1 gb:NM_006380.1	
	gb:NM_006773.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated) (DDX18), mRNA. /FEA=mrna /GEN=DDX18	
	/PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 /DB_XREF=gi:13787205 /UG=Hs.100555 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-	
	regulated) /FL-gb:NM_006773.2	
	Consensus includes gb:AF681579 /FEA=EST /DB_XREF=gi:4899032 /DB_XREF=est:tp93g08.x1 /CLONE=IMAGE:2206910 /UG=Hs.699 peptidylprolyl isom-	
	erase B (cyclophilin B)	
	Consensus includes gb:AL050091.1 /DEF=Homo sapiens mRNA; cDNA DKFp5564F1918 (from clone DKFp5564F1918), partial cds. /FEA=mrna	
	/GEN=DKFp5564F1918 /PROD=hypothetical protein /DB_XREF=gi:4884111 /UG=Hs.6283 DKFp5564F1918 protein	
	Consensus includes gb:BF224073 /FEA=EST /DB_XREF=gi:11131299 /DB_XREF=est:7q83e05.x1 /CLONE=IMAGE:3704936 /UG=Hs.278544 acetyl-Coenzyme A	
	acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	
	gb:NM_006153.1 /DEF=Homo sapiens NCK adaptor protein 1 (NCK1), mRNA. /FEA=mrna /GEN=NCK1 /PROD=NCK adaptor protein 1 /DB_XREF=gi:5453753 /	
	UG=Hs.54589 NCK adaptor protein 1 /FL-gb:NM_006153.1	

208860_s_at	gb:U09820.1 / DEF=Human helicase II (RAD54L) mRNA, complete cds. / FEA=mrna / GEN=RAD54L / PROD=helicase II / DB_XREF=gi:606832 / UG=Hs.96264 alpha thalassemia mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog) / FL=gb:U09820.1 gb:NM_000489.1 gb:U72937.2
203224_at	Consensus includes gb:BF340123 / FEA=EST / DB_XREF=gi:11286585 / DB_XREF=est:602037283F1 / CLONE=IMAGE:4185212 / UG=Hs.37558 hypothetical prote- in FLJ11149 / FL=gb:NM_018339.1
208619_at	gb:U40326.1 / DEF=Homo sapiens Hepatitis B virus X-associated protein 1 mRNA, complete cds. / FEA=mrna / PROD=X-associated protein 1 / DB_XREF=gi:695361 / UG=Hs.108327 damage-specific DNA binding protein 1 (127kD) / FL=gb:U18299.1 gb:NM_001923.2 gb:U40326.1 Consensus includes gb:NM_005826.1 / DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA. / FEA=CDS / GEN=HNRPR / PROD=heterogeneous nuclear ribonucleoprotein R / DB_XREF=gi:5031754 / UG=Hs.15265 heterogeneous nuclear ribonucleoprotein R / FL=gb:BC001449.1 gb:AF000364.1 gb:NM_005826.1
208765_s_at	gb:NM_016610.1 / DEF=Homo sapiens Toll-like receptor 8 (LOC51311), mRNA. / FEA=mrna / GEN=LOC51311 / PROD=Toll-like receptor 8 / DB_XREF=gi:7706147 /
220832_at	UG=Hs.27410 Toll-like receptor 8 / FL=gb:AF246971.1 gb:NM_016610.1 gb:AF245703.1 gb:NM_004865.1 / DEF=Homo sapiens TBP-like 1 (TBP1), mRNA. / FEA=mrna / GEN=TBPL1 / PROD=TBP-like 1 / DB_XREF=gi:4759233 / UG=Hs.13993 TBP-like 1 / FL=gb:AF130312.1 gb:NM_004865.1
208998_s_at	gb:NM_002643.1 / DEF=Homo sapiens phosphatidylinositol glycan, class F (PIGF), mRNA. / FEA=mrna / GEN=PIGF / PROD=phosphatidylinositol glycan, class F / DB_XREF=gi:4505796 / UG=Hs.166982 phosphatidylinositol glycan, class F / FL=gb:DI3435.1 gb:NM_002643.1
205077_s_at	gb:AB020712.1 / DEF=Homo sapiens mRNA for KIAA0905 protein, complete cds. / FEA=mrna / GEN=KIAA0905 / PROD=KIAA0905 protein / DB_XREF=gi:4240298 / UG=Hs.70266 yeast Sec31p homolog / FL=gb:AB020712.1
210616_s_at	gb:BC005975.1 / DEF=Homo sapiens, calcyclin binding protein; clone MGC:14660, mRNA, complete cds. / FEA=mrna / PROD=calcyclin binding protein / DB_XREF=gi:13543650 / FL=gb:BC005975.1
211761_s_at	Consensus includes gb:AI867198 / FEA=EST / DB_XREF=gi:5540214 / DB_XREF=est:wa01c11.x1 / CLONE=IMAGE:2296820 / UG=Hs.324787 solute carrier fam- ily 5 (inositol transporters), member 3 / FL=gb:NM_006933.1
213164_at	gb:NM_018386.1 / DEF=Homo sapiens hypothetical protein FLJ11305, mRNA. / FEA=mrna / GEN=FLJ11305 / PROD=hypothetical protein FLJ11305 / DB_XREF=gi:8922986 / UG=Hs.7049 hypothetical protein FLJ11305 / FL=gb:NM_018386.1
219940_s_at	Consensus includes gb:BG254653 / FEA=EST / DB_XREF=gi:12764469 / DB_XREF=est:602368621F1 / CLONE=IMAGE:4476773 / UG=Hs.247324 hypothetical pro- tein LOC63931 / FL=gb:NM_022100.1
203800_s_at	Consensus includes gb:BE965998 / FEA=EST / DB_XREF=gi:11770950 / DB_XREF=est:601659892R1 / CLONE=IMAGE:3905710 / UG=Hs.264482 Apq12 (autophagy 12, S. cerevisiae)-like
213026_at	Consensus includes gb:AL080099.1 / DEF=Homo sapiens mRNA; cDNA DKFp5564G1272 (from clone DKFp5564G1272); partial cds. / FEA=mrna / GEN=DKFp5564G1272 / PROD=hypothetical protein / DB_XREF=gi:5262522 / UG=Hs.2057 uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5-decarboxylase)
215165_x_at	gb:NM_003113.1 / DEF=Homo sapiens nuclear antigen Sp100 (SP100), mRNA. / FEA=mrna / GEN=SP100 / PROD=nuclear antigen Sp100 / DB_XREF=gi:4507164 / UG=Hs.77617 nuclear antigen Sp100 / FL=gb:M60618.1 gb:NM_003113.1
202864_s_at	gb:NM_001331.1 / DEF=Homo sapiens catenin (cadherin-associated protein), delta 1 (CTNND1), mRNA. / FEA=mrna / GEN=CTNND1 / PROD=catenin (cadherin-associated protein), delta 1 / DB_XREF=gi:10835009 / UG=Hs.166011 catenin (cadherin-associated protein), delta 1 / FL=gb:NM_001331.1
208407_s_at	gb:AF062317.1 gb:NM_002035.1 / DEF=Homo sapiens follicular lymphoma variant translocation 1 (FVTL), mRNA. / FEA=mrna / GEN=FVTL / PROD=follicular lymphoma variant translocation 1 / DB_XREF=gi:4503816 / UG=Hs.74050 follicular lymphoma variant translocation 1 / FL=gb:NM_002035.1
202419_at	gb:NM_001527.1 / DEF=Homo sapiens histone deacetylase 2 (HDAC2), mRNA. / FEA=mrna / GEN=HDAC2 / PROD=histone deacetylase 2 / DB_XREF=gi:4557640 / UG=Hs.3352 histone deacetylase 2 / FL=gb:U31814.1 gb:NM_001527.1
201833_at	Consensus includes gb:AL566824 / FEA=EST / DB_XREF=gi:12919571 / DB_XREF=est:AL566824 / CLONE=CSODF025YN03 (3 prime) / UG=Hs.172405 cell divi- sion cycle 27 / FL=gb:NM_001256.1
217879_at	

Tabelle 5: Gene aus Clusteranalyse 5

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der Genebank Datenbank
201466_s_at	gb:NM_002228.2 / DEF=Homo sapiens v-jun avian sarcoma virus 17 oncogene homolog / DB_XREF=gi:7710122 / UG=Hs.78465 v-jun avian sarcoma virus 17 oncogene homolog / FL=gb:BC002646.1 gb:NM_002228.2
202425_x_at	gb:NM_000944.1 / DEF=Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) [PPP3CA], mRNA. / FEA-mRNA / GEN=PPP3CA / PROD=protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) / DB_XREF=gi:6715567 / UG=Hs.272458 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) / FL=gb:J05480.1 gb:U14778.1
218566_s_at	gb:NM_012124.1 / DEF=Homo sapiens chord domain-containing protein 1 (CHP1), mRNA. / FEA-mRNA / GEN=CHP1 / PROD=chord domain-containing protein 1 / DB_XREF=gi:6912303 / UG=Hs.22857 cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 / FL=gb:AF192466.1
214349_at	Consensus includes gb:AV764378 / FEA=EST / DB_XREF=gi:10922226 / DB_XREF=est:AV764378 / CLONE=MDSAOE03 / UG=Hs.163863 ESTs, Moderately similar to POL2 HUMAN RETROVIRUS-RELATED POL POLYPROTEIN H. sapiens
204314_s_at	gb:NM_004379.1 / DEF=Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA. / FEA-mRNA / GEN=CREB1 / PROD=cAMP responsive element binding protein 1 / DB_XREF=gi:4758053 / UG=Hs.79194 cAMP responsive element binding protein 1 / FL=gb:M27691.1 gb:NM_004379.1
208753_s_at	gb:BC002387.1 / DEF=Homo sapiens, nucleosome assembly protein 1-like 1, clone MGC:8688, mRNA, complete cds. / FEA-mRNA / PROD=nucleosome assembly protein 1-like 1 / DB_XREF=gi:112803166 / UG=Hs.179662 nucleosome assembly protein 1-like 1 / FL=gb:BC002387.1 gb:AL162068.1
215452_x_at	Consensus includes gb:AL031133 / DEF=Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, S
204119_s_at	gb:U90339.1 / DEF=Human adenosine kinase short form mRNA, complete cds. / FEA-mRNA / PROD=adenosine kinase short form / DB_XREF=gi:1906010 / UG=Hs.94382 adenosine kinase / FL=gb:U50196.1 gb:BC003568.1 gb:U90339.1 gb:NM_001123.1
201304_at	gb:NM_005000.2 / DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kd, B13) (NDUFAS), nuclear gene encoding mitochondrial protein, mRNA. / FEA-mRNA / GEN=NDUFAS / PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 / DB_XREF=gi:13599821 / UG=Hs.83916 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kd, B13) / FL=gb:BC000813.1 gb:NM_005000.2 gb:U53468.1 gb:U64028.1
218131_s_at	gb:NM_017660.1 / DEF=Homo sapiens hypothetical protein FLJ20085 (FLJ20085), mRNA. / FEA-mRNA / GEN=FLJ20085 / PROD=hypothetical protein FLJ20085 / DB_XREF=gi:8923093 / UG=Hs.118964 hypothetical protein FLJ20085 / FL=gb:NM_017660.1
201788_at	gb:NM_007372.1 / DEF=Homo sapiens RNA helicase-related protein (RNAHP), mRNA. / FEA-mRNA / GEN=RNAHP / PROD=RNA helicase-related protein / DB_XREF=gi:11321631 / UG=Hs.8765 RNA helicase-related protein / FL=gb:NM_007372.1 gb:AF083255.1
209780_at	gb:AL136883.1 / DEF=Homo sapiens mRNA; cDNA DKFp434D166 (from clone DKFp434D166); complete cds. / FEA-mRNA / GEN=DKFp434D166 / PROD=hypothetical protein / DB_XREF=gi:12053266 / UG=Hs.128653 hypothetical protein DKFp434D166 / FL=gb:AL136883.1
219375_at	gb:NM_006090.1 / DEF=Homo sapiens cholineethanolaminephosphotransferase (CEPT1), mRNA. / FEA-mRNA / GEN=CEPT1 / PROD=cholineethanolaminephosphotransferase / DB_XREF=gi:5174414 / UG=Hs.125031 cholineethanolaminephosphotransferase / FL=gb:AF068302.1 gb:NM_006090.1
209187_at	Consensus includes gb:AW516932 / FEA=EST / DB_XREF=gi:7154941 / DB_XREF=est:xq04a05.x1 / CLONE=IMAGE-2748848 / UG=Hs.16697 down-regulator of transcription 1, TBP-binding (negative cofactor 2) / FL=gb:BC002809.1
219279_at	gb:NM_017718.1 / DEF=Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA. / FEA-mRNA / GEN=FLJ20220 / PROD=hypothetical protein FLJ20220 / DB_XREF=gi:8923209 / UG=Hs.21126 hypothetical protein FLJ20220 / FL=gb:NM_017718.1
206976_s_at	gb:NM_006644.1 / DEF=Homo sapiens heat shock 105kd (HSP105B), mRNA. / FEA-mRNA / GEN=HSP105B / PROD=heat shock 105kd / DB_XREF=gi:5729878 / UG=Hs.36927 heat shock 105kd / FL=gb:AB003333.1 gb:NM_006644.1
215596_s_at	Consensus includes gb:AL163248 / DEF=Homo sapiens chromosome 21 segment HS21C048 / FEA-mRNA_2 / DB_XREF=gi:7717304 / UG=Hs.288773 zinc finger protein 294

216511_s_at	Consensus includes gb:AJ270770 /DEF-Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exon 1 and joined CDS features / FEA-mRNA_1 / DB_XREF=gi:9188625 /UG=Hs.283857 Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exon 1 and joined CDS features
201889_at	gb:NM_014888.1 /DEF-Homo sapiens predicted osteoblast protein (GS3786), mRNA. /FEA-mRNA /GEN=GS3786 /PROD=predicted osteoblast protein / DB_XREF=gi:7661713 /UG=Hs.29882 predicted osteoblast protein /FL=gb:DB7120.1 gb:NM_014888.1
201435_s_at	Consensus includes gb:AM268640 /FEA-EST /DB_XREF=gi:6655670 /DB_XREF=est:xv52a03.x1 /CLONE=IMAGE:2816716 /UG=Hs.79306 eukaryotic translation initiation factor 4E /FL=gb:M15353.1 gb:NM_001968.1
212232_at	Consensus includes gb:AB023231.1 /DEF-Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA-mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein / DB_XREF=gi:4589677 /UG=Hs.6834 KIAA1014 protein
214329_x_at	Consensus includes gb:AM474434 /FEA-EST /DB_XREF=gi:7044540 /DB_XREF=est:xs95h07.x1 /CLONE=IMAGE:2777437 /UG=Hs.301527 ESTs, Moderately similar to unknown H.sapiens
212099_at	Consensus includes gb:AI263909 /FEA-EST /DB_XREF=gi:3872112 /DB_XREF=est:qi08f09.x1 /CLONE=IMAGE:1855913 /UG=Hs.204354 ras homolog gene family, member B /FL=gb:NM_004040.1
213618_at	Consensus includes gb:AB011152.1 /DEF-Homo sapiens mRNA for KIAA0580 protein, partial cds. /FEA-mRNA /GEN=KIAA0580 /PROD=KIAA0580 protein / DB_XREF=gi:3043683 /UG=Hs.22572 KIAA0580 protein
216899_s_at	Consensus includes gb:AC003999 /DEF-Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /FEA-mRNA /GEN=EIF4E /PROD=eukaryotic translation initiation factor 4E /DB_XREF=gi:4503534 /UG=Hs.79306 eukaryotic translation initiation factor 4E /FL=gb:M15353.1 gb:NM_001968.1
201437_s_at	Consensus includes gb:AW771590 /FEA-EST /DB_XREF=gi:7703647 /DB_XREF=est:hms8g08.x1 /CLONE=IMAGE:3032126 /UG=Hs.166982 phosphatidylinositol glycan, class F
212122_at	Consensus includes gb:BE866412 /FEA-EST /DB_XREF=gi:10315097 /DB_XREF=est:601678647F1 /CLONE=IMAGE:3961522 /UG=Hs.119222 suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting protein) /FL=gb:U1714.1 gb:AF116650.1
208666_s_at	Consensus includes gb:NM_018204.1 /DEF-Homo sapiens cytoskeleton associated protein 2 (CKAP2), mRNA. /FEA-mRNA /GEN=CKAP2 /PROD=cytoskeleton associated protein 2 /FL=gb:AL136848.1 gb:NM_018204.1
218252_at	Consensus includes gb:AF257099 /DEF-Homo sapiens prothymosin alpha (PTMA) gene, complete cds /FEA=CDS /DB_XREF=gi:8037944 /UG=Hs.283947 Homo sapiens prothymosin alpha (PTMA) gene, complete cds
216384_x_at	Consensus includes gb:AK026451.1 /DEF-Homo sapiens cDNA: FLJ22798 fis, clone KIAA2617. /FEA-mRNA /DB_XREF=gi:10439320 /UG=Hs.127287 KIAA0794 protein
217100_s_at	Consensus includes gb:AA161486 /FEA-EST /DB_XREF=gi:1735796 /DB_XREF=est:zq42d09.s1 /CLONE=IMAGE:632369 /UG=Hs.79194 cAMP responsive element binding protein 1 /FL=gb:M27691.1 gb:NM_004379.1
204313_s_at	Consensus includes gb:AA890010 /FEA-EST /DB_XREF=gi:3016889 /DB_XREF=est:aj89h08.s1 /CLONE=IMAGE:1403679 /UG=Hs.50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1
214257_s_at	Consensus includes gb:NM_018072.1 /DEF-Homo sapiens hypothetical protein FLJ10359 (FLJ10359), mRNA. /FEA-mRNA /GEN=FLJ10359 /PROD=hypothetical protein FLJ10359 /DB_XREF=gi:8922377 /UG=Hs.285861 hypothetical protein FLJ10359 /FL=gb:NM_018072.1
218595_s_at	Consensus includes gb:AA527499 /FEA-EST /DB_XREF=gi:2269568 /DB_XREF=est:ng41f07.s1 /CLONE=IMAGE:937381 /UG=Hs.301667 Homo sapiens mRNA, cDNA DKFZp566i043 (from clone DKFZp566i043)
213128_s_at	gb:NM_014812.1 /DEF-Homo sapiens KIAA0470 gene product (KIAA0470), mRNA. /FEA-mRNA /GEN=KIAA0470 /PROD=KARP-1-binding protein / DB_XREF=gi:7662141 /UG=Hs.25132 KIAA0470 gene product /FL=gb:AB022657.1 gb:NM_014812.1
207719_x_at	gb:BC001659.1 /DEF-Homo sapiens, RNA-binding protein S1, serine-rich domain, clone MGC:1125, mRNA, complete cds. /FEA-mRNA / PROD=RNA-binding protein S1, serine-rich domain /DB_XREF=gi:12804496 /UG=Hs.75104 RNA-binding protein S1, serine-rich domain
200060_s_at	FL=gb:BC001659.1 gb:BC001838.1
200634_at	gb:NM_005022.1 /DEF-Homo sapiens profilin 1 (PFN1); mRNA. /FEA-mRNA /GEN=PFN1 /PROD=profilin 1 /DB_XREF=gi:4826897 /UG=Hs.75721 profilin 1 / FL=gb:BC002475.1 gb:J03191.1 gb:NM_005022.1
202770_s_at	gb:NM_004354.1 /DEF-Homo sapiens cyclin G2 (CCNG2), mRNA. /FEA-mRNA /GEN=CCNG2 /PROD=cyclin G2 /DB_XREF=gi:4757935 /UG=Hs.79069 cyclin G2 / FL=gb:U4714.1 gb:NM_004354.1



201008_s_at	Consensus includes gb:AA812232 /FEA=EST /DB_XREF=gi:2881843 /DB_XREF=est:ob84h09.s1 /CLONE=IMAGE:1338113 /UG=Hs.179526 upregulated by 1,25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1 gb:873591.1
218534_s_at	gb:NM_018046.1 /DEF=Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA. /FEA=mrna /GEN=FLJ10283 /PROD=hypothetical protein FLJ10283 /DB_XREF=gi:8922325 /UG=Hs.284216 hypothetical protein FLJ10283 /FL=gb:NM_018046.1
200993_at	Consensus includes gb:AA939270 /FEA=EST /DB_XREF=gi:3099183 /DB_XREF=est:og31302.s1 /CLONE=IMAGE:1587915 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1
214102_at	Consensus includes gb:AK023737.1 /DEF=Homo sapiens cDNA FLJ13675 fis, clone PLACE1011875, highly similar to Homo sapiens mRNA for KIAA0580 protein. /FEA=mrna /DB_XREF=gi:10435758 /UG=Hs.287588 Homo sapiens cDNA FLJ13675 fis, clone PLACE1011875, highly similar to Homo sapiens mRNA for KIAA0580 protein
213704_at	Consensus includes gb:AA129753 /FEA=EST /DB_XREF=gi:1690163 /DB_XREF=est:z116a12.s1 /CLONE=IMAGE:502078 /UG=Hs.78948 Rab geranylgeranyl-trans-ferase, beta subunit
212367_at	Consensus includes gb:AI799061 /FEA=EST /DB_XREF=gi:5364533 /DB_XREF=est:we98a10.x1 /CLONE=IMAGE:2349114 /UG=Hs.6048 FEM-1 (C.elegans) homolog b /FL=gb:AF178632.1 gb:NM_015322.1 gb:AF204883.1
201873_s_at	gb:NM_002940.1 /DEF=Homo sapiens ATP-binding cassette, sub-family E (OABP), member 1 (ABCE1), mRNA. /FEA=mrna /GEN=ABCE1 /PROD=ATP-binding cassette, sub-family E, member 1 /DB_XREF=gi:4506558 /UG=Hs.12013 ATP-binding cassette, sub-family E (OABP), member 1 /FL=gb:NM_002940.1
218618_s_at	gb:NM_022763.1 /DEF=Homo sapiens hypothetical protein FLJ23399 (FLJ23399), mRNA. /FEA=mrna /GEN=FLJ23399 /PROD=hypothetical protein FLJ23399 /DB_XREF=gi:12232434 /UG=Hs.299883 hypothetical protein FLJ23399 /FL=gb:NM_022763.1
203689_s_at	Consensus includes gb:AI743037 /FEA=EST /DB_XREF=gi:5111325 /DB_XREF=est:wg85d05.x1 /CLONE=IMAGE:2371881 /UG=Hs.89764 fragile X mental retardation 1 /FL=gb:NM_002024.1
201074_at	Consensus includes gb:AA593983 /FEA=EST /DB_XREF=gi:2409333 /DB_XREF=est:nm16d01.s1 /CLONE=IMAGE:1084033 /UG=Hs.172280 SWISNP related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 /FL=gb:U66615.1 gb:NM_003074.1
200778_s_at	Consensus includes gb:AI191427 /FEA=EST /DB_XREF=gi:3742636 /DB_XREF=est:qe48g03.x1 /CLONE=IMAGE:1742260 /UG=Hs.155595 neural precursor cell expressed, developmentally down-regulated 5 /FL=gb:D28540.1 gb:NM_004404.1 gb:D63878.1
202307_s_at	gb:NM_000593.2 /DEF=Homo sapiens ATP-binding cassette, sub-family B (MDRTP), member 2 (ABCB2), mRNA. /FEA=mrna /GEN=ABCB2 /PROD=ATP-binding cassette, sub-family B, member 2 /DB_XREF=gi:9665247 /UG=Hs.158164 ATP-binding cassette, sub-family B (MDRTP), member 2 /FL=gb:I21204.1
213145_at	gb:L21205.1 gb:L21206.1 gb:L21207.1 gb:L21208.1 gb:NM_000593.2
218588_s_at	Consensus includes gb:BF001666 /FEA=EST /DB_XREF=gi:10701941 /DB_XREF=est:g91d12.x1 /CLONE=IMAGE:3313847 /UG=Hs.12460 Homo sapiens clone 23870 mRNA sequence
217834_s_at	gb:NM_018691.1 /DEF=Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA. /FEA=mrna /GEN=C5ORF3 /PROD=hypothetical protein /DB_XREF=gi:8922068 /UG=Hs.166551 chromosome 5 open reading frame 3 /FL=gb:NM_018691.1
205038_at	gb:NM_006372.1 /DEF=Homo sapiens NS1-associated protein 1 (NSAP1), mRNA. /FEA=mrna /GEN=NSAP1 /PROD=NS1-associated protein 1 /DB_XREF=gi:5453805 /UG=Hs.155489 NS1-associated protein 1 /FL=gb:AF155568.1 gb:NM_006372.1
203132_at	Consensus includes gb:BG540504 /FEA=EST /DB_XREF=gi:13532737 /DB_XREF=est:60556230f1 /CLONE=IMAGE:4693783 /UG=Hs.54452 zinc finger protein, subfamily 1A, 1 (Zkafos) /FL=gb:U40462.1 gb:NM_006060.1
211297_s_at	gb:NM_000321.1 /DEF=Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA. /FEA=mrna /GEN=RB1 /PROD=retinoblastoma 1 (including osteosarcoma) /DB_XREF=gi:4506434 /UG=Hs.75770 retinoblastoma 1 (including osteosarcoma) /FL=gb:M33647.1 gb:M15400.1 gb:M28419.1
212375_at	gb:NM_000321.1
208986_at	gb:L20320.1 /DEF=Human protein serine/threonine kinase stkl mRNA, complete cds. /FEA=mrna /PROD=protein serine/threonine kinase /DB_XREF=gi:348242 /UG=Hs.184298 cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) /FL=gb:L20320.1
217956_s_at	Consensus includes gb:AL563727 /FEA=EST /DB_XREF=gi:12913403 /DB_XREF=est:AL563727 /CLONE=CS0DD007YLL16 (3 prime) /UG=Hs.306094 trinucleotide repeat containing 12
214870_x_at	Consensus includes gb:AL559478 /FEA=EST /DB_XREF=gi:12905019 /DB_XREF=est:AL559478 /CLONE=CS0DD007YLL17 (5 prime) /UG=Hs.21704 transcription factor 12 (TF12), helix-loop-helix transcription factors 4 /FL=gb:M80627.1 gb:M83233.1 gb:NM_003205.2
209852_x_at	gb:NM_021204.1 /DEF=Homo sapiens E-1 enzyme (MASA), mRNA. /FEA=mrna /GEN=MASA /PROD=E-1 enzyme /DB_XREF=gi:10864016 /UG=Hs.18442 E-1 enzyme /FL=gb:NM_021204.1 gb:AF113125.1
	Consensus includes gb:AC002045 /DEF=Human Chromosome 16 BAC clone CIT987SK-A-589H1 /FEA=mrna_2 /DB_XREF=gi:2951945 /UG=Hs.251928 nuclear pore complex interacting protein
	gb:BC001423.1 /DEF=Homo sapiens, similar to proteasome (prosome, macropain) 28 subunit, 3, clone MGC:1394, mRNA, complete cds. /FEA=mrna /PROD=similar to proteasome (prosome, macropain) 28 subunit, 3 /DB_XREF=gi:12655138 /UG=Hs.152978 proteasome (prosome, macropain)

	activator subunit 3 (PA28 gamma; Ki) / FL=gb:BC001423.1 gb:BC002684.1	
	Consensus includes gb:BP248165 /FEA=EST /DB_XREF=gi:11164389 /DB_XREF=est:601859364F1 /CLONE=IMAGE:4069886 /UG=Hs.109643 polyadenylate	
209063_x_at	binding protein-interacting protein 1 /FL=gb:AL136920.1	
	gb:NM_005499.1 /DEF=Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA. /FEA=mrna /GEN=UBA2 /PROD=SUMO-1 activating enzyme subunit 2 /DB_XREF=gi:4885648 /UG=Hs.4311 SUMO-1 activating enzyme subunit 2 /FL=gb:BC003153.1 gb:AF090384.1 gb:AF079566.1	
201177_s_at	gb:AF110957.1 gb:NM_005499.1 gb:AL136905.1	
212264_s_at	Consensus includes gb:BE645850 /FEA=EST /DB_XREF=gi:9970161 /DB_XREF=est:7e7c03.x1 /CLONE=IMAGE:3288484 /UG=Hs.154978 KIAA0261 protein	
	gb:NM_012238.3 /DEF=Homo sapiens sirtuin (silent mating type information regulation 2, S. cerevisiae, homolog) 1 (SIRT1), mRNA. /FEA=mrna /GEN=SIRT1 /PROD=sirtuin 1 /DB_XREF=gi:13775598 /UG=Hs.31176 sirtuin (silent mating type information regulation 2, S. cerevisiae, homolog) 1 /FL=gb:NM_012238.3 gb:AF083106.2	
218878_s_at	gb:NM_004779.1 /DEF=Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA. /FEA=mrna /GEN=CNOT8 /PROD=CCR4-NOT transcription complex, subunit 8 /DB_XREF=gi:4758945 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1	
202163_s_at	gb:AF180476.1	
	gb:NM_014673.1 /DEF=Homo sapiens KIAA0103 gene product (KIAA0103), mRNA. /FEA=mrna /GEN=KIAA0103 /PROD=KIAA0103 gene product /DB_XREF=gi:7661909 /UG=Hs.154387 KIAA0103 gene product /FL=gb:D14659.1 gb:NM_014673.1	
203584_at	Consensus includes gb:214077.1 /DEF=H. sapiens mRNA for YY1NF-E1 protein. /FEA=mrna /PROD=YY1 NF-E1 /DB_XREF=gi:38010 /UG=Hs.97496 YY1	
201901_s_at	transcription factor /FL=gb:W7698.1 gb:W76541.1 gb:NM_003403.2	
213743_at	Consensus includes gb:BE674119 /FEA=EST /DB_XREF=gi:10034660 /DB_XREF=est:7d75b03.x1 /CLONE=IMAGE:3278765 /UG=Hs.155478 cyclin T2	
202883_s_at	Consensus includes gb:W79584 /FEA=EST /DB_XREF=gi:698093 /DB_XREF=est:Yd71a11.s1 /CLONE=IMAGE:113660 /UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FL=gb:NM_002716.1 gb:AF163473.1 gb:AF087438.1	
202069_s_at	Consensus includes gb:AI826060 /FEA=EST /DB_XREF=gi:5446731 /DB_XREF=est:wk28a12.x1 /CLONE=IMAGE:2413630 /UG=Hs.250616 isocitrate dehydrogenase 3 (NAD+) alpha /FL=gb:NM_005530.1 gb:U07681.1	
222303_at	Consensus includes gb:AV700891 /FEA=EST /DB_XREF=gi:10302862 /DB_XREF=est:AV700891 /CLONE=GRCEQD03 /UG=Hs.292477 ESTs	
	gb:NM_002408.2 /DEF=Homo sapiens mannosyl (alpha-1,6)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT2), mRNA. /FEA=mrna /GEN=MGAT2 /PROD=alpha-1,6-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase /DB_XREF=gi:6031183 /UG=Hs.172195 mannosyl (alpha-1,6)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase /FL=gb:NM_002408.2	
203102_s_at	Consensus includes gb:AI621223 /FEA=EST /DB_XREF=gi:4630349 /DB_XREF=est:ts77a09.x1 /CLONE=IMAGE:2237272 /UG=Hs.4014 KIAA0946 protein; Huntingtin interacting protein H	
212982_at	gb:NM_007145.1 /DEF=Homo sapiens zinc finger protein 146 (ZNF146), mRNA. /FEA=mrna /GEN=ZNF146 /PROD=zinc finger protein 146 /DB_XREF=gi:6005965 /UG=Hs.301819 zinc finger protein 146 /FL=gb:BC005154.1 gb:NM_007145.1	
200050_at	gb:NM_021105.1 /DEF=Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /FEA=mrna /GEN=PLSCR1 /PROD=phospholipid scramblase 1 /DB_XREF=gi:10863876 /UG=Hs.198282 phospholipid scramblase 1 /FL=gb:NM_021105.1 gb:AB006746.1 gb:AF098642.1	
202430_s_at	gb:NM_023010.1 /DEF=Homo sapiens similar to yeast Upf3, variant B (UPF3B), mRNA. /FEA=mrna /GEN=UPF3B /PROD=similar to yeast Upf3, variant B /DB_XREF=gi:12711673 /UG=Hs.103832 similar to yeast Upf3, variant B /FL=gb:AY013251.1 gb:NM_023010.1	
218757_s_at	Consensus includes gb:BE501352 /FEA=EST /DB_XREF=gi:9703760 /DB_XREF=est:7a41e05.x1 /CLONE=IMAGE:3221312 /UG=Hs.23294 ESTs, weakly similar to T15138 hypothetical protein T28F2.4 - Caenorhabditis elegans C.elegans	
214030_at	Consensus includes gb:BE501352 /FEA=EST /DB_XREF=gi:9703760 /DB_XREF=est:7a41e05.x1 /CLONE=IMAGE:3221312 /UG=Hs.23294 ESTs, weakly similar to T15138 hypothetical protein T28F2.4 - Caenorhabditis elegans C.elegans	
218093_s_at	gb:NM_017664.1 /DEF=Homo sapiens hypothetical protein FLJ20093 (FLJ20093), mRNA. /FEA=mrna /GEN=FLJ20093 /PROD=hypothetical protein FLJ20093 /DB_XREF=gi:8923103 /UG=Hs.172572 hypothetical protein FLJ20093 /FL=gb:NM_017664.1	
	Consensus includes gb:BF195973 /FEA=EST /DB_XREF=gi:11083411 /DB_XREF=est:7088c12.x1 /CLONE=IMAGE:3643391 /UG=Hs.102708 DRF2P34A043 protein /FL=gb:NM_015396.1	
203486_s_at	gb:NM_024546.1 /DEF=Homo sapiens hypothetical protein FLJ13449 (FLJ13449), mRNA. /FEA=mrna /GEN=FLJ13449 /PROD=hypothetical protein FLJ13449 /DB_XREF=gi:13375708 /UG=Hs.10711 hypothetical protein FLJ13449 /FL=gb:AL136651.1 gb:NM_024546.1	
219303_at	gb:NM_007146.1 /DEF=Homo sapiens zinc finger protein 161 (ZNF161), mRNA. /FEA=mrna /GEN=ZNF161 /PROD=zinc finger protein 161 /DB_XREF=gi:6005967 /UG=Hs.6557 zinc finger protein 161 /FL=gb:D28118.1 gb:NM_007146.1	
202173_s_at	Consensus includes gb:AK022697.1 /DEF=Homo sapiens cDNA FLJ12635 fis, clone NT2RM4001865, highly similar to Homo sapiens mRNA for atopy related autoantigen CALC. /FEA=mrna /DB_XREF=gi:10434244 /UG=Hs.61628 calcium binding atopy-related autoantigen 1	
216903_s_at		



205842_s_at	gb:AF001362.1 / DEF=Homo sapiens Jak2 kinase (JAK2) mRNA, complete cds. / FEA=mrna / GEN=JAK2 / PROD=JAK2 kinase / DB_XREF=gi:3236321 / UG=Hs.115541 Janus kinase 2 (a protein tyrosine kinase) / FL=gb:NM_004972.2 gb:AF005216.1 gb:AF058925.1 gb:AF001362.1
212702_s_at	Consensus includes gb:N45111 / FEA=EST / DB_XREF=gi:1186277 / DB_XREF=est:yz12f12.s1 / CLONE=IMAGE:282863 / UG=Hs.330988 Homo sapiens, similar to Bicaudal D (Drosophila) homolog 1, clone IMAGE:3622452, mRNA, partial cds
201664_at	gb:AL136877.1 / DEF=Homo sapiens mRNA: cDNA DKFp434F205 (from clone DKFp434F205); complete cds. / FEA=mrna / GEN=DKFp434F205 / PROD=hypothetical protein / DB_XREF=gi:6807670 / UG=Hs.50758 SMCA (structural maintenance of chromosomes 4, yeast)-like 1 / FL=gb:AB019987.1 gb:NM_005496.1 gb:AL136877.1
202060_at	gb:NM_014633.1 / DEF=Homo sapiens KIAA0155 gene product (KIAA0155), mRNA. / FEA=mrna / GEN=KIAA0155 / PROD=KIAA0155 gene product / DB_XREF=gi:7661949 / UG=Hs.173288 KIAA0155 gene product / FL=gb:NM_014633.1 gb:D63875.1
203177_x_at	gb:NM_003201.1 / DEF=Homo sapiens transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1), mRNA. / FEA=mrna / GEN=TCF6L1 / PROD=transcription factor 6-like 1 (mitochondrial transcription factor 1-like) / DB_XREF=gi:4507400 / UG=Hs.75133 transcription factor 6-like 1 (mitochondrial transcription factor 1-like) / FL=gb:M62810.1 gb:NM_003201.1
209748_at	gb:AB029006.1 / DEF=Homo sapiens mRNA for KIAA1083 protein, complete cds. / FEA=mrna / GEN=KIAA1083 / PROD=KIAA1083 protein / DB_XREF=gi:5689502 / UG=Hs.26334 spastic paraplegia 4 (autosomal dominant; spastin) / FL=gb:AB029006.1
200660_at	gb:NM_005620.1 / DEF=Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. / FEA=mrna / GEN=S100A11 / PROD=S100 calcium-binding protein A11 / DB_XREF=gi:5032056 / UG=Hs.256290 S100 calcium-binding protein A11 (calgizzarin) / FL=gb:D49355.1 gb:BC001410.1 gb:DS0374.1 gb:NM_005620.1 gb:D38583.1
222119_s_at	Consensus includes gb:AL117620.1 / DEF=Homo sapiens mRNA: cDNA DKFp564K2364 (from clone DKFp564K2364); partial cds. / FEA=mrna / GEN=DKFp564K2364 / PROD=hypothetical protein / DB_XREF=gi:5912200 / UG=Hs.284289 vitiligo-associated protein VIT-1
208934_s_at	gb:AF342815.1 / DEF=Homo sapiens colorectal carcinoma-derived galectin-8 variant 1 mRNA, complete cds. / FEA=mrna / PROD=colorectal carcinoma-derived galectin-8 variant 1 / DB_XREF=gi:13249298 / UG=Hs.4082 lectin, galactoside-binding, soluble, 8 (galectin 8) / FL=gb:AF342815.1 gb:L78132.1 gb:AF074000.1 gb:NM_006499.1
211698_at	gb:AF349444.1 / DEF=Homo sapiens Rb- and p300-binding protein EID-1 mRNA, complete cds. / FEA=mrna / PROD=Rb- and p300-binding protein EID-1 / DB_XREF=gi:13549113 / FL=gb:AF349444.1
212053_at	Consensus includes gb:AK025504.1 / DEF=Homo sapiens cDNA: FLJ21851 fis, clone HEP01962. / FEA=mrna / DB_XREF=gi:10438041 / UG=Hs.170218 KIAA0251 protein
209174_s_at	gb:BC000978.2 / DEF=Homo sapiens, hypothetical protein FLJ20259, clone MGC:5396, mRNA, complete cds. / FEA=mrna / PROD=hypothetical protein FLJ20259 / DB_XREF=gi:12803027 / UG=Hs.9956 hypothetical protein FLJ20259 / FL=gb:BC000978.2 gb:NM_017730.1
203476_at	gb:NM_006670.1 / DEF=Homo sapiens 5T4 oncofetal trophoblast glycoprotein (5T4), mRNA. / FEA=mrna / GEN=5T4 / PROD=5T4 oncofetal trophoblast glycoprotein / DB_XREF=gi:5729717 / UG=Hs.82128 5T4 oncofetal trophoblast glycoprotein / FL=gb:NM_006670.1
203007_x_at	gb:AF077198.1 / DEF=Homo sapiens lysophospholipase mRNA, complete cds. / FEA=mrna / PROD=lysophospholipase / DB_XREF=gi:4679009 / UG=Hs.12540 lysophospholipase I / FL=gb:AF081281.1 gb:AF077198.1 gb:NM_006330.1 gb:AF291053.1
212721_at	Consensus includes gb:AL810380 / FEA=EST / DB_XREF=gi:5396946 / DB_XREF=est:wb87h10.x1 / CLONE=IMAGE:2312707 / UG=Hs.47274 Homo sapiens mRNA: cDNA DKFp564B176 (from clone DKFp564B176)
218461_at	gb:NM_016301.1 / DEF=Homo sapiens protein x 0004 (LOC51184), mRNA. / FEA=mrna / GEN=LOC51184 / PROD=protein x 0004 / DB_XREF=gi:9994188 / UG=Hs.284164
214218_s_at	Consensus includes gb:AV699347 / FEA=EST / DB_XREF=gi:10301318 / DB_XREF=est:AV699347 / CLONE=GKCBPH07 / UG=Hs.83623 nuclear receptor subfamily 1, group I, member 3
218178_s_at	gb:NM_020412.1 / DEF=Homo sapiens CHMP1.5 protein (CHMP1.5), mRNA. / FEA=mrna / GEN=CHMP1.5 / PROD=CHMP1.5 protein / DB_XREF=gi:9966900 / UG=Hs.42733
217851_s_at	CHMP1.5 protein / FL=gb:AF281064.1 gb:NM_020412.1
202329_at	gb:NM_016045.1 / DEF=Homo sapiens CGI-107 protein (LOC51012), mRNA. / FEA=mrna / GEN=LOC51012 / PROD=CGI-107 protein / DB_XREF=gi:7705609 / UG=Hs.3945 CGI-107 protein / FL=gb:AF151865.1 gb:NM_016045.1
203302_at	gb:NM_004383.1 / DEF=Homo sapiens c-src tyrosine kinase (CSK), mRNA. / FEA=mrna / GEN=CSK / PROD=c-src tyrosine kinase / DB_XREF=gi:4758077 / UG=Hs.77793 c-src tyrosine kinase / FL=gb:NM_004383.1
201949_x_at	gb:NM_000788.1 / DEF=Homo sapiens deoxycytidine kinase (DCK), mRNA. / FEA=mrna / GEN=DCK / PROD=deoxycytidine kinase / DB_XREF=gi:4503268 / UG=Hs.709 deoxycytidine kinase / FL=gb:M60527.1 gb:NM_000788.1
	Consensus includes gb:AL572341 / FEA=EST / DB_XREF=gi:12930514 / DB_XREF=est:AL572341 / CLONE=CSOD1007YCL3 (3 prime) / UG=Hs.76368 capping pro-tein (actin filament) muscle 2-line, beta / FL=gb:NM_004930.1 gb:U03271.1

28

	lysosomal (vacuolar proton pump) 42kD. /FL=gb:NM_001695.1	
	Consensus includes gb:AF131748.1 /DEF-Homo sapiens clone 25191 GTP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA sequence, partial cds. /FEA-mRNA /PROD-GTP-specific succinyl-CoA synthetase betasubunit /DB_XREF=gi:4406563 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit	
214835_s_at	gb:AF082283.1 /DEF-Homo sapiens CARD-containing apoptotic signaling protein (BCL10) mRNA, complete cds. /FEA-mRNA /GEN=BCL10 /PROD=CARD-containing apoptotic signaling protein /DB_XREF=gi:4092066 /UG=Hs.193516 B-cell CLL/lymphoma 10 /FL=gb:AF082283.1	
205263_at	gb:AF057700.1 gb:AF100338.1 gb:NM_003921.1 gb:AF127386.1 gb:AF134395.1 gb:AF105066.1	
218512_at	gb:NM_018256.1 /DEF-Homo sapiens hypothetical protein FLJ10881 (FLJ10881), mRNA. /FEA-mRNA /GEN=FLJ10881 /PROD=hypothetical protein FLJ10881 /DB_XREF=gi:8922736 /UG=Hs.73291 hypothetical protein FLJ10881 /FL=gb:AF242546.1 gb:NM_018256.1	
210283_x_at	gb:BC005295.1 /DEF-Homo sapiens, similar to polyadenylate binding protein-interacting protein 1, clone MGC:12360, mRNA, complete cds. /FEA-mRNA /PROD=Similar to polyadenylate binding protein-interacting protein 1 /DB_XREF=gi:13529010 /UG=Hs.109643 polyadenylate binding protein-interacting protein 1 /FL=gb:BC005295.1	
202724_s_at	gb:NM_002015.2 /DEF-Homo sapiens forkhead box O1A (rhodomyosarcoma) /FL=gb:AF032885.1 gb:U02310.1 gb:NM_002015.2	
212058_at	gb:NM_002015.2 /DEF-Homo sapiens forkhead box O1A (rhodomyosarcoma) /FL=gb:AF032885.1 gb:U02310.1 gb:NM_002015.2	
212006_at	Consensus includes gb:AF1184562 /FEA-EST /DB_XREF=gi:3735200 /DB_XREF=est:q660505.x1 /CLONE=IMAGE:1733841 /UG=Hs.7976 KIAA0332 protein domain-containing 1	
222040_at	Consensus includes gb:AF1144007 /FEA-EST /DB_XREF=gi:3665816 /DB_XREF=est:q333c06.x1 /CLONE=IMAGE:1698058 /UG=Hs.249495	
202373_s_at	gb:AF225648.1 /DEF-Homo sapiens rGAP-iso mRNA, complete cds. /FEA-mRNA /PROD=rGAP-iso /DB_XREF=gi:12005820 /UG=Hs.197289 rab3 GTPase-activating protein, non-catalytic subunit (150kD) /FL=gb:AF255648.1 gb:AF004828.1 gb:NM_012414.1	
209301_at	gb:M36532.1 /DEF-Human carbonic anhydrase II mRNA, complete cds. /FEA-mRNA /GEN=CA2 /DB_XREF=gi:179794 /UG=Hs.155097 carbonic anhydrase II /FL=gb:J03037.1 gb:M36532.1 gb:NM_000067.1	
212364_at	Consensus includes gb:AW025150 /FEA-EST /DB_XREF=gi:5878680 /DB_XREF=est:wu94e06.x1 /CLONE=IMAGE:2527714 /UG=Hs.211601 mitogen-activated protein kinase kinase 12	
202863_at	gb:NM_003113.1 /DEF-Homo sapiens nuclear antigen Sp100 (SP100), mRNA. /FEA-mRNA /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FL=gb:M0618.1 gb:NM_003113.1	
217679_x_at	Consensus includes gb:AF1683552 /FEA-EST /DB_XREF=gi:4893734 /DB_XREF=est:tx67h02.x1 /CLONE=IMAGE:2274675 /UG=Hs.201605 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	
212802_s_at	Consensus includes gb:AK021841.1 /DEF-Homo sapiens cDNA FLJ13779 fls, clone PLACE4000445, highly similar to Homo sapiens mRNA DKFZp434C212 (from clone DKFZp434C212). /FEA-mRNA /DB_XREF=gi:10435900 /UG=Hs.172069 DKFZp434C212 protein	
210346_s_at	gb:AF212224.1 /DEF-Homo sapiens CLK4 mRNA, complete cds. /FEA-mRNA /PROD=CLK4 /DB_XREF=gi:9437514 /UG=Hs.295231 Homo sapiens CLK4 mRNA, complete cds. /FL=gb:AF212224.1	
208848_at	gb:M30471.1 /DEF-Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds. /FEA-mRNA /GEN=ADH5 /PROD=alcohol dehydrogenase 3 /DB_XREF=gi:178133 /UG=Hs.78989 alcohol dehydrogenase 5 (class III), chi polypeptide /FL=gb:NM_000671.2 gb:M29872.1 gb:M30471.1	
221978_at	Consensus includes gb:BE138825 /FEA-EST /DB_XREF=gi:8601325 /DB_XREF=est:xw96a07.x1 /CLONE=IMAGE:2835828 /UG=Hs.110309 major histocompatibility complex, class I, F	
217526_at	Consensus includes gb:AI478300 /FEA-EST /DB_XREF=gi:4371526 /DB_XREF=est:tm39e01.x1 /CLONE=IMAGE:2160504 /UG=Hs.192789 ESTs, weakly similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	
218322_s_at	gb:NM_016234.2 /DEF-Homo sapiens long-chain fatty acid coenzyme A ligase 5 (FACL5), mRNA. /FEA-mRNA /GEN=FACL5 /PROD=long-chain fatty acid coenzyme A ligase 5 /DB_XREF=gi:12669912 /UG=Hs.11638 long-chain fatty acid coenzyme A ligase 5 /FL=gb:NM_016234.2 gb:AB033899.1	
212613_at	Consensus includes gb:AI991252 /FEA-EST /DB_XREF=gi:5838157 /DB_XREF=est:wu41e09.x1 /CLONE=IMAGE:2522632 /UG=Hs.87497 butyrophilin, subfamily 3, member A2	
204566_at	gb:NM_003620.1 /DEF-Homo sapiens protein phosphatase 1D magnesium-dependent, delta isoform (PP1D), mRNA. /FEA-mRNA /GEN=PP1D /PROD=protein phosphatase 1D magnesium-dependent, delta isoform /DB_XREF=gi:4505996 /UG=Hs.100980 protein phosphatase 1D magnesium-dependent, delta isoform /FL=gb:U78305.1 gb:NM_003620.1	

Tabelle 6: Gene aus Clusteranalyse 6

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der Genebank Datenbank
202018_s_at	gb:NM_002343.1 / DEF=Homo sapiens lactotransferrin (LTF), mRNA. / FEA=mrna / GEN=LTF / PROD=lactotransferrin / DB_XREF=gi:4505042 / UG=Hs.105938 lactotransferrin / FL=gb:AF332168.1 gb:H93150.1 gb:M83202.1 gb:NM_002343.1
216379_x_at	Consensus includes gb:AK000168.1 / DEF=Homo sapiens cDNA FL20161 f1s, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA. / FEA=mrna / DB_XREF=gi:7020079 / UG=Hs.332045 Homo sapiens cDNA FL20161 f1s, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA
209771_x_at	Consensus includes gb:AA761181 / FEA=EST / DB_XREF=gi:2810111 / DB_XREF=est:nz0903.s1 / CLONE=IMAGE:1287316 / UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) / FL=gb:X69397.1
206676_at	gb:M33326.1 / DEF=Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds. / FEA=mrna / GEN=NCA / PROD=non-specific cross reacting antigen / B_XREF=gi:189101 / UG=Hs.41 carcinoembryonic antigen-related cell adhesion molecule 8 / FL=gb:M33326.1 gb:NM_001816.1
210254_at	gb:L35848.1 / DEF=Homo sapiens IGE receptor beta chain (HTM4) mRNA, complete cds. / FEA=mrna / GEN=HTM4 / PROD=Ige receptor beta subunit / DB_XREF=gi:561638 / UG=Hs.99960 membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific) / FL=gb:NM_006138.1 gb:L35848.1
203887_s_at	gb:NM_000361.1 / DEF=Homo sapiens thrombomodulin (THBD), mRNA. / FEA=mrna / GEN=THBD / PROD=thrombomodulin / DB_XREF=gi:4507482 / UG=Hs.2030 thrombomodulin / FL=gb:M16552.1 gb:NM_000361.1
212768_s_at	Consensus includes gb:AL390736 / DEF=Human DNA sequence from clone RP11-209119 on chromosome 13 Contains ESTs, STSs and GSSs. Contains the gene for the GW112 protein with two isoforms (GW112 and KIAA4294) / FEA=mrna / DB_XREF=gi:11182238 / UG=Hs.273321 differentially expressed in hematopoietic lineages
202887_s_at	gb:NM_019058.1 / DEF=Homo sapiens hypothetical protein (FLJ20500), mRNA. / FEA=mrna / GEN=FLJ20500 / PROD=hypothetical protein / DB_XREF=gi:19506686 / UG=Hs.111244 hypothetical protein / FL=gb:AL136668.1 gb:NM_019058.1
200916_at	gb:NM_003564.1 / DEF=Homo sapiens transgelin 2 (TAGLN2), mRNA. / FEA=mrna / GEN=TAGLN2 / PROD=transgelin 2 / DB_XREF=gi:4507356 / UG=Hs.75725 transgelin 2 / FL=gb:D21261.1 gb:NM_003564.1
206157_at	gb:NM_002852.1 / DEF=Homo sapiens pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA. / FEA=mrna / GEN=PTX3 / PROD=pentaxin-related gene, rapidly induced by IL-1 beta / DB_XREF=gi:4506332 / UG=Hs.2050 pentaxin-related gene, rapidly induced by IL-1 beta / FL=gb:M31166.1 gb:NM_002852.1
209369_at	gb:M63310.1 / DEF=Human 1,2-cyclic-inositol-phosphate phosphodiesterase (ANX3) mRNA, complete cds. / FEA=mrna / GEN=ANX3 / PROD=1,2-cyclic-inositol-phosphate phosphodiesterase / DB_XREF=gi:178696 / UG=Hs.1378 annexin A3 / FL=gb:BC000871.1
202497_x_at	Consensus includes gb:AI631159 / FEA=EST / DB_XREF=gi:4682489 / DB_XREF=est:ts93d05.x1 / CLONE=IMAGE:2238825 / UG=Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3 / FL=gb:M20681.1 gb:NM_006931.1
205513_at	gb:NM_001062.1 / DEF=Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA. / FEA=mrna / GEN=TCN1 / PROD=transcobalamin I (vitamin B12 binding protein, R binder family) / DB_XREF=gi:4507406 / UG=Hs.2012 transcobalamin I (vitamin B12 binding protein, R binder family) / FL=gb:J05068.1 gb:NM_001062.1
206697_s_at	gb:NM_005143.1 / DEF=Homo sapiens haptoglobin (HP), mRNA. / FEA=mrna / GEN=HP / PROD=haptoglobin / DB_XREF=gi:4826761 / UG=Hs.75990 haptoglobin / FL=gb:K00422.1 gb:L29394.1 gb:NM_005143.1
202146_at	Consensus includes gb:AA747426 / FEA=EST / DB_XREF=gi:2787384 / DB_XREF=est:nx8e08.s1 / CLONE=IMAGE:1269350 / UG=Hs.7879 interferon-related developmental regulator 1 / FL=gb:BC001272.1 gb:NM_001550.1
266_s_at	L33930 / FEA=FEATRE= / DEF=INTITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region
211657_at	gb:M18728.1 / DEF=Human nonspecific crossreacting antigen mRNA, complete cds. / FEA=mrna / GEN=NCA; NCA; NCA / PROD=non-specific cross reacting antigen / DB_XREF=gi:189084 / FL=gb:M18728.1

205214_at	gb:NM_004226.1 / DEF=Homo sapiens serine/threonine kinase 17b (apoptosis-inducing) (STK17B), mRNA. / FEA=mrna / GEN=STK17B / PROD=serine/threonine kinase 17b (apoptosis-inducing) / DB_XREF=gi:4758193 / UG=Hs.120996 serine/threonine kinase 17b (apoptosis-inducing) / FL=gb:AB011421.1 gb:NM_004226.1
207574_s_at	gb:NM_015675.1 / DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. / FEA=mrna / GEN=GADD45B / PROD=DRF2P566B133 protein / DB_XREF=gi:9945331 / UG=Hs.110571 growth arrest and DNA-damage-inducible, beta / FL=gb:AF090950.1 gb:NM_015675.1
206343_s_at	gb:NM_013959.1 / DEF=Homo sapiens neurogranin 1 (NRG1), transcript variant SMDF, mRNA. / FEA=mrna / GEN=NRG1 / PROD=neurogranin 1 isoform SMDF // DB_XREF=gi:7669517 / UG=Hs.172816 neurogranin 1 / FL=gb:NM_013959.1 gb:L41827.1
214146_s_at	Consensus includes gb:R64130 / FEA=EST / DB_XREF=gi:836009 / DB_XREF=est:y118h03.s1 / CLONE=IMAGE:139637 / UG=Hs.2164 pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
215716_s_at	Consensus includes gb:L14561 / DEF=Homo sapiens plasma membrane calcium ATPase, Ca++ transporting, plasma membrane 1 splice products, partial cds / FEA=mrna.2 / DB_XREF=gi:4165324 / UG=Hs.78546 ATPase, Ca++ transporting, plasma membrane 1
201179_s_at	gb:J03005.1 / DEF=Human alternative guanine nucleotide-binding regulatory protein (G) alpha-inhibitory-subunit mRNA, complete cds. / FEA=mrna / GEN=GNAT1 / DB_XREF=gi:183183 / UG=Hs.73799 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 / FL=gb:J03005.1 gb:J03198.1 gb:M27543.1 gb:J03238.1 gb:NM_006496.1
201626_at	Consensus includes gb:BG292233 / FEA=EST / DB_XREF=gi:13050848 / DB_XREF=est:602386668f1 / CLONE=IMAGE:451521 / UG=Hs.56205 insulin induced gene 1 / FL=gb:NM_005542.1
209728_at	gb:BC005312.1 / DEF=Homo sapiens, clone MGC:12387, mRNA, complete cds. / FEA=mrna / PROD=Unknown (protein for MGC:12387) / DB_XREF=gi:13529055 / UG=Hs.318720 Homo sapiens, clone MGC:12387, mRNA, complete cds / FL=gb:BC005312.1 gb:M16942.1
212665_at	Consensus includes gb:AL556438 / FEA=EST / DB_XREF=gi:12899113 / DB_XREF=est:AL556438 / CLONE=CS00K004Y118 (3 prime) / UG=Hs.12813 DMF2P4340216 protein
200665_s_at	gb:NM_003118.1 / DEF=Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA. / FEA=mrna / GEN=SPARC / PROD=secreted protein, acidic, cysteine-rich (osteonectin) / DB_XREF=gi:4507170 / UG=Hs.111779 secreted protein, acidic, cysteine-rich (osteonectin) / FL=gb:BC004974.1 gb:J03040.1 gb:NM_003118.1
201407_s_at	Consensus includes gb:AI186712 / FEA=EST / DB_XREF=gi:3737350 / DB_XREF=est:qe82f01.x1 / CLONE=IMAGE:1745497 / UG=Hs.21537 protein phosphatase 1, catalytic subunit, beta isoform / FL=gb:NM_002709.1 gb:AF092905.1
203505_at	gb:AF285167.1 / DEF=Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, complete cds. / FEA=mrna / GEN=ABCA1 / PROD=ATP-binding cassette transporter 1 / DB_XREF=gi:9755158 / UG=Hs.211562 ATP-binding cassette, sub-family A (ABCA1), member 1 / FL=gb:AF165281.1 gb:NM_005502.1 gb:AF285167.1
221802_s_at	Consensus includes gb:AUI57109 / FEA=EST / DB_XREF=gi:11018630 / DB_XREF=est:AUI57109 / CLONE=FLAC1006159 / UG=Hs.23740 KIAA1598 protein
201844_s_at	Consensus includes gb:W84482 / FEA=EST / DB_XREF=gi:1395613 / DB_XREF=est:zdb9h07.s1 / CLONE=IMAGE:356701 / UG=Hs.7910 RING1 and YY1 binding protein / FL=gb:AF179286.1 gb:AB029551.1 gb:NM_012234.1
206390_x_at	gb:NM_002619.1 / DEF=Homo sapiens platelet factor 4 (PF4), mRNA. / FEA=mrna / GEN=PF4 / PROD=platelet factor 4 / DB_XREF=gi:4505732 / UG=Hs.81564 platelet factor 4 / FL=gb:M25897.1 gb:NM_002619.1
212569_at	Consensus includes gb:AV699744 / FEA=EST / DB_XREF=gi:10301715 / DB_XREF=est:AV699744 / CLONE=GKCEDF05 / UG=Hs.8118 KIAA0650 protein
211960_s_at	Consensus includes gb:BG261416 / FEA=EST / DB_XREF=gi:12771232 / DB_XREF=est:602373192f1 / CLONE=IMAGE:4484422 / UG=Hs.237955 hypothetical protein PRO2706
202422_s_at	gb:NM_002977.1 / DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA. / FEA=mrna / GEN=PACLA / PROD=long-chain fatty-acid-Coenzyme A ligase, long-chain 4, isoform 2 / DB_XREF=gi:12669908 / UG=Hs.81452 fatty-acid-Coenzyme A ligase, long-chain 4 / FL=gb:NM_002977.1
221958_s_at	Consensus includes gb:AA775681 / FEA=EST / DB_XREF=gi:2835015 / DB_XREF=est:zf31a02.s1 / CLONE=IMAGE:378506 / CLONE=IMAGE:378506
204621_s_at	Consensus includes gb:AI935096 / FEA=EST / DB_XREF=gi:5673966 / DB_XREF=est:wp13e10.x1 / CLONE=IMAGE:2464746 / UG=Hs.82120 nuclear receptor subfamily 4, group A, member 2 / FL=gb:NM_006186.1
201409_s_at	gb:NM_002709.1 / DEF=Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), mRNA. / FEA=mrna / GEN=PPP1CB / PROD=protein phosphatase 1, catalytic subunit, beta isoform / DB_XREF=gi:4506004 / UG=Hs.21537 protein phosphatase 1, catalytic subunit, beta isoform / FL=gb:NM_002709.1 gb:AF092905.1

201662_s_at	gb:ID89053.1 /DEF=Homo sapiens mRNA for Acyl-CoA-synthetase 3, complete cds. /FEA=mRNA /PROD=Acyl-CoA synthetase 3 /DB_XREF=gi:4165017 /UG=Hs.268012 fatty-acid-Coenzyme A ligase, long-chain 3 /FL=gb:NM_004457.2 gb:ID89053.1 gb:AF116690.1
220987_s_at	gb:NM_030952.1 /DEF=Homo sapiens hypothetical protein DKFZp434J037 (DKFZp434J037), mRNA. /FEA=mRNA /GEN=DKFZp434J037 /PROD=hypothetical protein DKFZp434J037 /DB_XREF=gi:13569921 /FL=gb:NM_030952.1
219607_s_at	gb:NM_024021.1 /DEF=Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4), mRNA. /FEA=mRNA /GEN=MS4A4 /PROD=membrane-spanning 4-domains, subfamily A, member 4 /DB_XREF=gi:13430865 /UG=Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 /FL=gb:AB013102.1 b:NM_024021.1 gb:AF068288.1 gb:NM_016650.1
201565_s_at	gb:NM_002166.1 /DEF=Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA. /FEA=mRNA /GEN=ID2 /PROD=inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /DB_XREF=gi:4504570 /UG=Hs.180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /FL=gb:M7796.1 gb:NM_002166.1 gb:DI3891.1
213327_s_at	Consensus includes gb:AI820101 /FEA=EST /DB_XREF=gi:5439180 /DB_XREF=est:wg56d12.x1 /CLONE=IMAGE:236911 /UG=Hs.42400 ubiquitin specific protease 12
203603_s_at	gb:NM_014795.1 /DEF=Homo sapiens zinc finger homeobox 1B (ZFHX1B), mRNA. /FEA=mRNA /GEN=ZFHX1B /PROD=zinc finger homeobox 1B /DB_XREF=gi:7662183 /UG=Hs.34871 zinc finger homeobox 1B /FL=gb:AB011141.1 gb:NM_014795.1
217963_s_at	gb:NM_014380.1 /DEF=Homo sapiens p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) (DXS6984E), mRNA. /FEA=mRNA /GEN=DXS6984E /PROD=p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) /DB_XREF=gi:7657043 /UG=Hs.17775 p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) /FL=gb:NM_014380.1 gb:AF187064.1
206710_s_at	gb:NM_012307.1 /DEF=Homo sapiens differentially expressed in adenocarcinoma of the lung (KIAA0987), mRNA. /FEA=mRNA /GEN=KIAA0987 /PROD=differentially expressed in adenocarcinoma of the lung /DB_XREF=gi:6912469 /UG=Hs.103839 erythrocyte membrane protein band 4.1-like 3 /FL=gb:AF069072.1 gb:NM_012307.1
204342_at	gb:NM_013386.1 /DEF=Homo sapiens hypothetical protein (DKFZp586G0123); mRNA. /FEA=mRNA /GEN=DKFZp586G0123 /PROD=hypothetical protein /DB_XREF=gi:9358726 /UG=Hs.24713 hypothetical protein /FL=gb:AL050209.1 gb:NM_013386.1
204393_s_at	gb:NM_001099.2 /DEF=Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /FEA=mRNA /GEN=ACPP /PROD=prostatic acid phosphatase precursor /DB_XREF=gi:6382063 /UG=Hs.1852 acid phosphatase, prostate /FL=gb:M24902.1 gb:M34840.1 gb:NM_001099.2
200719_at	Consensus includes gb:BE964043 /FEA=EST /DB_XREF=gi:11767371 /DB_XREF=est:601657616R1 /CLONE=IMAGE:3875955 /UG=Hs.171626 transcription elongation factor B (SIII), polypeptide 1-like /FL=gb:NM_003197.2
202731_at	gb:NM_014456.1 /DEF=Homo sapiens programmed cell death 4 (PDCD4), mRNA. /FEA=mRNA /GEN=PDCD4 /PROD=programmed cell death 4 /DB_XREF=gi:7657448 /UG=Hs.296251 programmed cell death 4 /FL=gb:U96628.1 gb:NM_014456.1
204094_s_at	gb:NM_014779.1 /DEF=Homo sapiens KIAA0669 gene product /FL=gb:AB014569.1 gb:NM_014779.1 /DB_XREF=gi:7662235 /UG=Hs.52526 KIAA0669 gene product /FL=gb:AB014569.1 gb:NM_014779.1
208690_s_at	gb:BC000915.1 /DEF=Homo sapiens, Similar to LIM protein; clone MGC:5344, mRNA, complete cds. /FEA=mRNA /PROD=Similar to LIM protein /DB_XREF=gi:12654194 /UG=Hs.75807 PDZ and LIM domain 1 (elfin) /FL=gb:BC000915.1
208979_at	gb:AF128458.1 /DEF=Homo sapiens nuclear receptor coactivator RAP250 mRNA, complete cds. /FEA=mRNA /PROD=nuclear receptor coactivator RAP250 /DB_XREF=gi:7140573 /UG=Hs.159613 thyroid hormone receptor binding protein /FL=gb:AF177388.1 gb:AF208227.1 gb:AF128458.1 gb:NM_014071.1 gb:AF171667.1 gb:AF245115.1
201772_at	gb:NM_015878.1 /DEF=Homo sapiens antizyme inhibitor (LOC51582), mRNA. /FEA=mRNA /GEN=LOC51582 /PROD=antizyme inhibitor /DB_XREF=gi:7706219 /UG=Hs.223014 antizyme inhibitor /FL=gb:D88674.1 gb:NM_015878.1
201345_s_at	gb:NM_003339.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2D-2 (homologous to yeast UBC45) (UBE2D2), mRNA. /FEA=mRNA /GEN=UBE2D2 /PROD=ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /DB_XREF=gi:4507774 /UG=Hs.108332 ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /FL=gb:U39317.1 gb:NM_003339.1
221060_s_at	gb:NM_003266.1 /DEF=Homo sapiens toll-like receptor 4 (TLR4), mRNA. /FEA=mRNA /GEN=TLR4 /PROD=toll-like receptor 4 /DB_XREF=gi:4507532 /UG=Hs.159239 toll-like receptor 4 /FL=gb:U88880.1 gb:NM_003266.1
208878_s_at	gb:AF092132.1 /DEF=Homo sapiens PAK2 mRNA, complete cds. /FEA=mRNA /PROD=PAK2 /DB_XREF=gi:5138913 /UG=Hs.284275 Homo sapiens PAK2 mRNA, 7complete cds /FL=gb:AF092132.1
212628_at	Consensus includes gb:BG292055 /FEA=EST /DB_XREF=gi:13050507 /DB_XREF=est:602386350F1 /CLONE=IMAGE:4515036 /UG=Hs.69171 protein kinase C-like 2
212928_at	Consensus includes gb:AL050331 /DEF=Human DNA sequence from clone 48613 on chromosome 6q22.1-22.3. Contains the part of a gene for a novel protein, the gene for KIAA0721 (NAP (Nucleosome Assembly Protein))

	domain containing protein); the TSPYL gene for TSPYL-like (testis specific protei... /FEA=RNA_1
	/DB_XREF=gi:566855 /UG=Hs.284141 KIAA0721 protein /FL=gb:NM_021648.1
	gb:AF090900.1 /DEF=Homo sapiens clone HQ0189 PRO0189 mRNA, complete cds. /FEA=RNA /PROD=PRO0189
	/DB_XREF=gi:6690176 /UG=Hs.91393 Homo sapiens cDNA: FLJ21887 fls, clone HEP03135,
221568_s_at	highly similar to AF090900 Homo sapiens clone HQ0189 PRO0189 mRNA /FL=gb:AF090900.1
	Consensus includes gb:W67887 /FEA=EST /DB_XREF=gi:1376776 /DB_XREF=est:z438c11.s1 /CLONE=IMAGE:342932
201408_at	/UG=Hs.21537 protein phosphatase 1, catalytic subunit, beta isoform /FL=gb:NM_002709.1 gb:AF092905.1
	gb:NM_002053.1 /DEF=Homo sapiens guanylate binding protein 1, interferon-inducible, 67kD (GBP1), mRNA.
202270_at	/FEA=RNA /GEN=GBP1 /PROD=guanylate binding protein 1, interferon-inducible, 67kD /DB_XREF=gi:4503938
	UG=Hs.62661 guanylate binding protein 1, interferon-inducible, 67kD /FL=gb:BC002666.1 gb:M55542.1 gb:NM_002053.1
	gb:NM_012290.1 /DEF=Homo sapiens tousled-like kinase 1 (TLKL), mRNA. /FEA=RNA /GEN=TLKL /PROD=tousled-like kinase 1
202606_s_at	/DB_XREF=gi:6912719 /UG=Hs.18895 tousled-like kinase 1 /FL=gb:AB004885.1 gb:NM_012290.1 gb:AF246219.1
	Consensus includes gb:AA664011 /FEA=EST /DB_XREF=gi:2618002 /DB_XREF=est:ac03f10.s1 /CLONE=IMAGE:855403
216037_x_at	/UG=Hs.173638 transcription factor 7- like 2 (T-cell specific, HMG-box)
	gb:L21934.2 /DEF=Homo sapiens acyl-coenzyme A: cholesterol acyltransferase mRNA, complete cds.
221561_at	/FEA=RNA /PROD=acyl-coenzyme A: cholesterol acyltransferase /DB_XREF=gi:4878021
	/UG=Hs.14553 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 /FL=gb:NM_003101.1 gb:L21934.2
203680_at	gb:NM_002736.1 /DEF=Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA.
	/FEA=RNA /GEN=PRKAR2B /PROD=protein kinase, cAMP-dependent, regulatory, type II, beta /DB_XREF=gi:4506064
	/UG=Hs.77439 protein kinase, cAMP-dependent, regulatory, type II, beta /FL=gb:M31158.1 gb:NM_002736.1
	Consensus includes gb:AK027071.1 /DEF=Homo sapiens cDNA: FLJ23418 fls, clone HEP21245,
215111_s_at	highly similar to HS035048 Human TSC-22 protein mRNA. /FEA=RNA /DB_XREF=gi:10440100
	/UG=Hs.114360 transforming growth factor beta-stimulated protein TSC-22
	gb:BC005122.1 /DEF=Homo sapiens, ADP-ribosylation factor GTPase activating protein 1,
202211_at	clone MGC:10272, mRNA, complete cds. /FEA=RNA /
	PROD=ADP-ribosylation factor GTPase activating protein 1 /DB_XREF=gi:13477296 /UG=Hs.13014 ADP-ribosylation factor GTPase activating
	protein 1 /FL=gb:BC005122.1 gb:AF111847.1 gb:NM_014570.1
221918_at	Consensus includes gb:AI742210 /FEA=EST /DB_XREF=gi:5110498 /DB_XREF=est:wg39c02.x1 /CLONE=IMAGE:2367458 /UG=Hs.183302 ESTs
	Consensus includes gb:AV712064 /FEA=EST /DB_XREF=gi:10731370 /DB_XREF=est:AV712064 /CLONE=DCAUD05 /UG=Hs.9456 SWISNF related, matrix
213251_at	associated,
	actin dependent regulator of chromatin, subfamily a, member 5
209186_at	gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=RNA /GEN=HK1 /DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++
	transporting, cardiac muscle, slow twitch 2 /FL=gb:M23114.1
210996_s_at	gb:U43430.1 /DEF=Human epsilon isoform 14-3-3 protein mRNA, complete cds. /FEA=RNA /PROD=14-3-3 protein /DB_XREF=gi:4096944 /UG=Hs.79474
	tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, epsilon polypeptide /FL=gb:U43399.1 gb:U43430.1
	Consensus includes gb:AA873600 /FEA=EST /DB_XREF=gi:2969722 /DB_XREF=est:ob12a02.s1 /CLONE=IMAGE:1323434 /UG=Hs.42945 acid sphingomyeli-
213624_at	nase-
	like phosphodiesterase
	gb:NM_003157.1 /DEF=Homo sapiens serinethreonine kinase 2 (STK2), mRNA. /FEA=RNA /GEN=STK2 /PROD=serinethreonine kinase 2
204634_at	/DB_XREF=gi:4507276 /
	UG=Hs.1087 serinethreonine kinase 2 /FL=gb:L20321.1 gb:NM_003157.1
212515_s_at	Consensus includes gb:BG492602 /FEA=EST /DB_XREF=gi:13454114 /DB_XREF=est:602536568F1 /CLONE=IMAGE:4655296 /UG=Hs.147916 DEADH
	(Asp-Glu-Ala-AspHis) box polypeptide 3
218170_at	gb:NM_016048.1 /DEF=Homo sapiens CGI-111 protein (LOC51015), mRNA. /FEA=RNA /GEN=LOC51015 /PROD=CGI-111 protein /DB_XREF=gi:7705613 /
	UG=Hs.11085 CGI-111 protein /FL=gb:AF151869.1 gb:NM_016048.1
	gb:BC005032.1 /DEF=Homo sapiens, Sec23 (S. cerevisiae) homolog B, clone MGC:12666, mRNA, complete cds. /FEA=RNA /PROD=Sec23 (S. cerevi-
210293_s_at	siae)
	homolog B /DB_XREF=gi:13477148 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /FL=gb:BC005032.1
221493_at	gb:AL136629.1 /DEF=Homo sapiens mRNA: cDNA DKFp564D152 (from clone DKFp564D152); complete cds. /FEA=RNA /GEN=DKFp564D152 /
	PROD=hypothetical protein /DB_XREF=gi:12052783 /UG=Hs.278479 TSPY-like /FL=gb:AL136629.1



213506_at	Consensus includes gb:BE965369 /FEA=EST /DB_XREF=gi:11769659 /DB_XREF=est:601659282R1 /CLONE=IMAGE:3895653 /UG=Hs.168102 Human proteinase activated receptor-2 mRNA, 3UTR
201016_at	Consensus includes gb:BE542684 /FEA=EST /DB_XREF=gi:9771329 /DB_XREF=est:601067180F1 /CLONE=IMAGE:3453571 /UG=Hs.4310 eukaryotic translation initiation factor 1A /FL=gb:BC000793.1 gb:NM_001412.1
203414_at	gb:NM_012329.1 /DEF=Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA. /FEA=mrna /GEN=MMD /PROD=monocyte to macrophage differentiation-associated, precursor /DB_XREF=gi:6912507 /UG=Hs.79889 monocyte to macrophage differentiation-associated /FL=gb:NM_012329.1
213510_x_at	Consensus includes gb:AW194543 /FEA=EST /DB_XREF=gi:6473381 /DB_XREF=est:xb27c02.x1 /CLONE=IMAGE:2577506 /UG=Hs.234573 Homo sapiens mRNA for
218539_at	FLJ20725 /gb:NM_017943.1 /DEF=Homo sapiens hypothetical protein FLJ20725 (FLJ20725), mRNA. /FEA=mrna /GEN=FLJ20725 /PROD=hypothetical protein FLJ20725 /DB_XREF=gi:8923650 /UG=Hs.15467 hypothetical protein FLJ20725 /FL=gb:NM_017943.1
218172_s_at	gb:NM_018630.1 /DEF=Homo sapiens hypothetical protein PRO2577 /FL=gb:AF116708.1 gb:NM_018630.1
202538_s_at	DB_XREF=gi:8924181 /UG=Hs.241576 hypothetical protein PRO2577 /FL=gb:AF116708.1 gb:NM_018630.1
221504_s_at	gb:NM_014043.1 /DEF=Homo sapiens DKFZP5640123 protein (DKFZP5640123), mRNA. /FEA=mrna /GEN=DKFZP5640123 /PROD=DKFZP5640123 protein /DB_XREF=gi:7661633 /UG=Hs.11449 DKFZP5640123 protein /FL=gb:AF151842.1 gb:AL080122.1 gb:NM_014043.1
	gb:AF112204.1 /DEF=Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA, complete cds. /FEA=mrna /PROD=Vacuolar proton pump subunit
	SFD alpha isoform /DB_XREF=gi:6563195 /UG=Hs.19575 CGI-11 protein /FL=gb:AF298777.1 gb:AF132945.1 gb:AF112204.1 gb:NM_015941.1
	Consensus includes gb:AB011139.1 /DEF=Homo sapiens mRNA for KIAA0567 protein, partial cds. /FEA=mrna /GEN=KIAA0567 /PROD=KIAA0567 protein
212213_x_at	/
216652_s_at	DB_XREF=gi:3043657 /UG=Hs.147946 optic atrophy 1 (autosomal dominant)
221472_at	Consensus includes gb:AL137673.1 /DEF=Homo sapiens mRNA; cDNA DKFZp344H0872 (from clone DKFZp344H0872). /FEA=mrna /DB_XREF=gi:6807841 /UG=Hs.306454 Homo sapiens mRNA; cDNA DKFZp344H0872 (from clone DKFZp344H0872)
	Consensus includes gb:Z97053 /DEF=Human DNA sequence from clone RPL-179W20 on chromosome 20 Contains a 3 end of a novel gene similar to cellular retinaldehyde-binding protein, the TDE1 gene (tumour differentially expressed 1), the PKTG gene encoding protein kinase (cAMP-dependent... /
	FEA=mrna_2 /DB_XREF=gi:9650676 /UG=Hs.272168 tumor differentially expressed 1 /FL=gb:U49188.1 gb:AF112227.1 gb:AF153979.1 gb:NM_006811.1
212526_at	Consensus includes gb:AK002207.1 /DEF=Homo sapiens cDNA FLJ11345 fis, clone PLACE1010877, highly similar to Homo sapiens mRNA for KIAA0610
200624_s_at	protein. /FEA=mrna /DB_XREF=gi:7023938 /UG=Hs.118087 KIAA0610 protein
201091_s_at	Consensus includes gb:AA577695 /FEA=EST /DB_XREF=gi:2355879 /DB_XREF=est:nn22h02.s1 /CLONE=IMAGE:1084659 /UG=Hs.78825 matrix 3 /FL=gb:NM_018834.1 gb:AB018266.1
217863_at	Consensus includes gb:BE748755 /FEA=EST /DB_XREF=gi:10162747 /DB_XREF=est:601571933T1 /CLONE=IMAGE:3838737 /UG=Hs.278554 heterochromatin-like protein 1 /FL=gb:AF136630.1 gb:NM_016587.1
202804_at	Consensus includes gb:AI348378 /FEA=EST /DB_XREF=gi:4085584 /DB_XREF=est:qg20h06.x1 /CLONE=IMAGE:1909115 /UG=Hs.75251 DEADH (Asp-Glu-Ala-AspHis)
	Box binding protein 1 /FL=gb:AF077951.1 gb:AF167160.1 gb:NM_016166.1
	Consensus includes gb:AI539710 /FEA=EST /DB_XREF=gi:4453845 /DB_XREF=est:tp77b05.x1 /CLONE=IMAGE:2205297 /UG=Hs.89433 ATP-binding cassette, sub-family C (CFTR/ATP), member 1 /FL=gb:U05628.1 gb:NM_004996.2
	Consensus includes gb:AU150824 /FEA=EST /DB_XREF=gi:11012345 /DB_XREF=est:AU150824 /CLONE=NT2RF2003689 /UG=Hs.2491 DiGeorge syndrome critical
214198_s_at	region gene 2
217976_s_at	gb:NM_016141.1 /DEF=Homo sapiens dynein light chain-A (LOC51143), mRNA. /FEA=mrna /GEN=LOC51143 /PROD=dynein light chain-A /DB_XREF=gi:7705852 /



	UG=Hs.266483 dynein light chain-A /FL=gb:AF078849.1 gb:NM_016141.1	
202318_s_at	gb:AF306508.1 /DEF=Homo sapiens SUMO-1 specific protease FKSG6 mRNA, complete cds. /FEA=mrna /PROD=SUMO-1 specific protease FKSG6 /DB_XREF=gi:11096243 /UG=Hs.27197 SUMO-1-specific protease /FL=gb:AF307849.1 gb:AF306508.1 gb:AF196304.1 gb:NM_015571.1 gb:AF107405.1 /DEF=Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds. /FEA=mrna /GEN=SFRS3 /PROD=pre-mRNA splicing factor	
208673_s_at	DB_XREF=gi:5531903 /UG=Hs.167460 splicing factor, arginineserine-rich 3 /FL=gb:BC000914.1 gb:AF107405.1 gb:NM_022771.1 /DEF=Homo sapiens hypothetical protein FLJ12085 (FLJ12085), mRNA. /FEA=mrna /GEN=FLJ12085 /PROD=hypothetical protein	
218268_at	DB_XREF=gi:12232450 /UG=Hs.48827 hypothetical protein FLJ12085 /FL=gb:NM_022771.1 gb:BC000961.2 /DEF=Homo sapiens, degenerative spermatocyte (homolog Drosophila; lipid desaturase), clone MGC:5079, mRNA, complete cds. /FEA=mrna /PROD=degenerative spermatocyte (homolog Drosophila; lipid desaturase) /DB_XREF=gi:12803018 /UG=Hs.185973 degenerative spermatocyte (homolog Drosophila; lipid desaturase) /FL=gb:AF132963.1 gb:NM_015957.1	
209250_at	(homolog Drosophila; lipid desaturase) /FL=gb:BC000961.2	
218698_at	gb:NM_015957.1 /DEF=Homo sapiens CGI-29 protein (LOC51074), mRNA. /FEA=mrna /GEN=LOC51074 /PROD=CGI-29 protein /DB_XREF=gi:7705723 /UG=Hs.104058 CGI-29 protein	

## Patentansprüche

1. Array bestehend aus Oligo- oder Polynukleotidsonden,  
~~die immobilisiert auf einem festen Träger aufge-~~  
5       bracht sind, dadurch gekennzeichnet, dass auf der  
Oberfläche Sequenzen einer Auswahl oder aller der  
in den Tabellen 1-6 genannten selektiven Monozyten-  
Makrophagen-Gene gebunden sind.
- 10       2. Array nach Anspruch 1, dadurch gekennzeichnet, dass  
gegebenenfalls zusätzlich weitere Gene verwendet  
werden, von denen bekannt ist, dass sie in jeder  
Zelle exprimiert werden und zur Grundausstattung  
einer Zelle gehören.
- 15       3. Array nach Anspruch 1 und 2, dadurch gekennzeichnet,  
dass mit den genannten Genen komplementäre RNA auf  
der Oberfläche des Arrays gebunden ist zum inversen  
Nachweis über die in den Tabellen 1-6 dargestellten  
20       Gene oder Gensequenzen.
4. Array nach Anspruch 1 bis 3, dadurch gekennzeichnet,  
dass die Gene, deren Teil- und Oligomersequenzen  
krankheits- und nebenwirkungsrelevante selektio-  
nierte Gene der rheumatoiden Arthritis oder anderer  
chronisch entzündlichen Erkrankungen vor und nach  
anti-TNF-Therapie sind.
- 25       5. Array nach Anspruch 1 bis 4, dadurch gekennzeichnet,  
dass die Gene, deren Teilsequenzen und Oligomer-  
sequenzen krankheitsspezifisch regulierte Gene des  
Monozyten/Makrophagen-Zellsystems sind.
- 30

6. Array nach Anspruch 1 bis 5, dadurch gekennzeichnet, dass auf der Oberfläche gegebenenfalls auch Allele, Derivate und/oder Splicingvarianten der Gen- bzw. Genteilsequenzen und Oligomersequenzen vorliegen.
- 

5

7. Array nach Anspruch 1 bis 6, dadurch gekennzeichnet, dass es auf der Oberfläche Gensequenzen enthält, die mindestens eine Teil-Sequenzidentität von 80 % in den Protein-kodierenden Abschnitten der mRNA besitzen.

10

8. Array nach Anspruch 1 bis 7, dadurch gekennzeichnet, dass die Oberfläche der Träger mit reaktiven Gruppen, Metallverbindungen oder Legierungen beschichtet ist.

15

9. Array nach Anspruch 1 bis 8, dadurch gekennzeichnet, dass die Gene oder Gensequenzen durch Spottingverfahren von cDNA, Immobilisierungsverfahren und Syntheseverfahren von Oligomeren oder spiegelbildlich in Form von RNA aufgebracht sind.

20

10. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, die zum Nachweis Fluoreszenzfarbstoff-, Enzym-, Protein- oder radioaktiv markiert sind und eine Verstärkung zulassen.

25

11. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, dadurch gekennzeichnet, dass die Verstärkung der Signale über gekoppelte alkalische Phosphatase, Peroxidase, Biotin Digoxigenin-, Proteinmoleküle, (Edel-)Metallchelate oder Beads erfolgt.

30

12. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, dadurch gekennzeichnet, dass zur zusätzlichen Verstärkung der Signale Streptavidin, (Edel-)Metall-chelate, Beads oder Antikörper eingesetzt werden.
- 

5

13. Verwendung des Arrays nach Anspruch 1 bis 9 zum inversen Nachweis festphasengebundener Total-RNA oder messenger-RNA.

10

14. Verwendung des Arrays nach Anspruch 1 bis 9 zur Messung der Monozyten/Makrophagen-Aktivierung oder der Entzündungsaktivität im Blut oder im Zellgewebe.

15

15. Verwendung des Arrays nach Anspruch 1 bis 9 zur Feindiagnostik sowie zur Früherkennung von entzündlichen Erkrankungen und der rheumatoiden Arthritis.

20

16. Verwendung des Arrays nach Anspruch 1 bis 9 zur Verfolgung von Nebenwirkungen bei der anti-TNF-Therapie von entzündlichen Erkrankungen und der rheumatoiden Arthritis.

25

17. Verwendung des Arrays nach Anspruch 1 bis 9 zur Überwachung der Therapie und Erstellung einer Prognose bei entzündlichen Erkrankungen und der rheumatoiden Arthritis.

30

18. Verwendung der Arrays nach Anspruch 1 bis 9 zur Identifizierung von pharmazeutischen Targets bei entzündlichen Erkrankungen und der rheumatoiden Arthritis.

19. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6 zu Einzelgennachweisverfahren, vorzugsweise reverse Transkriptions-PCR (RT-PCR):
- 

- 5 20. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6, dadurch gekennzeichnet, dass sie mit einer Markierung oder einer Reporterfunktion ausgestattet sind.
- 10 21. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6 zum reversen Nachweis festphasengebundener Total-RNA oder messenger-RNA in einem RNA-Array mit bis zu 500 Gewebs- und/oder Blutproben.

## Zusammenfassung

Die Erfindung betrifft einen Array bestehend aus Oligo-

5 oder Polynukleotidsonden, die immobilisiert auf einen festen Träger aufgebracht sind. Das Array ist dadurch charakterisiert, dass auf der Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1-6 genannten selektiven Monozyten-Makrophagen-Gene gebunden sind. Das  
10 Array ermöglicht die Diagnose der rheumatoiden Arthritis und anderer chronisch entzündlicher Erkrankungen, eine begleitende Analyse der Behandlungseffektivität und die Überwachung von Nebenwirkungen bei der anti-Tumornekrosefaktor (TNF)-Therapie und somit die Auswahl  
15 der für den jeweiligen Patienten mit rheumatoider Arthritis am wirkungsvollsten Therapie. Die vorliegende Erfindung betrifft ferner einen Nukleinsäure-Array zur Prognose und zur Entwicklung neuer anti-TNF gerichteter Pharmaka oder solcher Pharmaka, die in dessen Regelkreis eingreifen.  
20

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